

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 24, 2004, 03:55:11 ; Search time 2708 Seconds
(without alignments)
1776.235 Million cell updates/sec

Title: US-10-613-105-2

Perfect score: 762

Sequence: 1 MKSSGLFPFLVLLALGLTAP.....RDLKCCMGCKSCVSPVKA 132

Scoring table:

BLOSUM62	Xgapop 10.0 , Xgapext 0.5
-DB-EST -OPMT-fastap	-SUFFIX=rat -MINMATCH=0.1 -LOP=0.1 -LOPEXT=0
Xgapop 10.0 , Ygapext 0.5	
Xgapop 6.0 , Ygapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-O=/cgn2_1/USPTO_spool_h/US10613105/runat_22102004_170441_18696/app_query.fasta_1.327
-DB-EST -OPMT-fastap -SUFFIX=rat -MINMATCH=0.1 -LOP=0.1 -LOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=100
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=45 -MODE=LOCAL
-OUTFMT=ptc -NOR=ext -HEA=SIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10613105@CGN 1 3437 @runat_22102004_170441_18696 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	762	100.0	477	1	AA460433
2	762	100.0	534	4	BI490742
3	762	100.0	535	4	BM769596
4	762	100.0	543	6	CD690842
5	762	100.0	554	6	CD070973
6	762	100.0	563	5	BX089446
7	762	100.0	583	7	CK430164
8	762	100.0	593	4	BM767014
9	762	100.0	597	4	BM843274

10	762	100.0	599	6	CD000587
11	762	100.0	603	7	CK429948
12	762	100.0	606	4	BM842052
13	762	100.0	612	5	BM976429
14	762	100.0	626	5	BQ232871
15	762	100.0	760	6	CD103997
16	762	100.0	796	6	CD000527
17	762	100.0	874	4	BG533465
18	758	99.5	394	9	AY417768
19	758	99.5	537	7	CF529326
20	758	99.5	598	5	BM753561
21	758	99.5	599	6	CB305723
22	758	99.5	607	7	CF529317
23	758	99.5	623	6	CD685198
24	757	99.3	524	6	CD689844
25	757	99.3	589	5	BQ436671
26	757	99.3	608	4	BI253834
27	757	99.3	610	6	CD108133
28	757	99.3	612	6	CB152458
29	757	99.3	906	5	BQ631723
30	756	99.2	541	6	CD690425
31	756	99.2	582	1	AA572950
32	754	99.0	582	6	CD690400
33	754	99.0	633	5	BU927919
34	748	98.2	433	4	BM694343
35	748	98.2	567	4	BM704851
36	748	98.2	962	4	BI489624
37	747	98.0	575	2	AW264225
38	746	97.9	580	6	CB151317
39	740	97.1	483	2	BE396187
40	738	96.9	581	2	BE320800
41	734	96.3	557	2	BE743613
42	734	96.3	583	4	BI189626
43	733	96.2	770	4	BG484664
44	728	95.5	793	2	BE271401
45	726	95.3	511	6	CD699640
46	726	95.3	634	4	BG617592
47	726	95.3	940	4	BG675719
48	722	94.8	493	6	CD683966
49	721	94.6	560	2	BQ38352
50	720	94.5	447	4	BM708788
51	717	94.1	584	1	AI638119
52	716	94.0	582	1	AI885550
53	713	93.6	394	9	AY417769
54	713	93.6	587	1	AI862145
55	710	93.2	464	1	AA132992
56	706	92.7	738	2	BQ36845
57	703	92.3	528	1	AA683520
58	703	92.3	560	2	AW238407
59	696	91.3	484	2	BE184455
60	691.5	90.7	568	1	AI743345
61	691	90.7	548	6	CD723292
62	687	90.2	991	2	BE788273
63	686	90.0	697	7	CO579827
64	685	89.9	439	1	AA316675
65	685	89.9	469	4	BM708085
66	685	89.9	553	5	BU731938
67	684.5	89.8	561	1	AI742512
68	680	89.2	537	2	AW081599
69	676	88.7	548	5	BU730356
70	673.5	88.4	451	2	BF896911
71	672	88.2	505	2	BE612943
72	672	88.2	519	2	BE612494
73	672	88.2	584	1	AI564623
74	672	88.2	739	4	BG537787
75	667	87.5	575	1	AA587140
76	664	87.1	486	7	R71834
77	664	87.1	886	4	BG547643
78	663	87.0	572	1	AI222907
79	662.5	86.9	572	1	AA564454
80	662	86.9	550	5	BU731488
81	657	86.2	560	1	AA551908
82	655	86.2	566	1	AA541595

LOCUS CD690842 543 bp mRNA linear EST 25-JUN-2003
DEFINITION EST7365 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION CD690842
VERSION CD690842.1 GI:32211980
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 543)
AUTHORS Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and Zeng,Y.-X.
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: Yixin Zeng
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Fax: 86-20-8775-4506
Email: yxzeng@zsuns.edu.cn.

FEATURES
source
1..543
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/notes="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

ORIGIN
Alignment Scores:
Pred. No.: 3,34e-60 Length: 543
Score: 762.00 Matches: 132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-613-105-2 (1-132) x CD690842 (1-543)

Qy 1 MetLysSerSerGlyLeuPheProPheValLeuLeuAlaLeuGlyThrLeuAlaPro 20
Db 53 ATGAGTCCAGCGCCCTCTCCCTTCTGGTGTGCTGGCTGGGAATCTGGCACT 112
Qy 21 TrpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProProLysLysSer 40
Db 113 TGGGCTGTGGAAGGCTCTGGAAGTCTTCAAAGCTGGAGTCTGCTCTCTAAGAAATCT 172
Qy 41 AlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAspTyrGlnCysProGlyLys 60
Db 173 GCCCAGTGCCTTATGATACAAAGAACCTGAGTGCAGAGTGAATGCTGAGTGCAGGAAG 232
Qy 61 LysArgCysCysProAspThrCysGlyLysLysCysLeuAspProValAspThrProAsn 80
Db 233 AAGAGATGTTGCTCTGACACTTGTGGCATCAAATGCTGATCTGTTGACACCCCAAC 292
Qy 81 ProThrArgArgLysProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAsn 100
Db 293 CCAACAAGGAGGAAGCTCGGAAGTGCAGTGCCTGATCTATGGCCAATGTTGATGCTTAAC 352
Qy 101 ProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGly 120
Db 353 CCCCCCAATTCTGTGATGATGATGGCCAGTGCAGGCGTGAATGATGATGATGGGC 412
Qy 121 MetCysGlyLysSerCysValSerProValLysAla 132
Db 413 ATGTGTGGGAAATCTCGGTTTCCCTGTGGAAGCT 448

RESULT 5
CD707973
LOCUS

DEFINITION EST24500 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION CD707973
VERSION CD707973.1 GI:32238603
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 554)
AUTHORS Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and Zeng,Y.-X.
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: Yixin Zeng
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Fax: 86-20-8775-4506
Email: yxzeng@zsuns.edu.cn.

FEATURES
source
1..554
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/notes="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

ORIGIN
Alignment Scores:
Pred. No.: 3,43e-60 Length: 554
Score: 762.00 Matches: 132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-613-105-2 (1-132) x CD707973 (1-554)

Qy 1 MetLysSerSerGlyLeuPheProPheValLeuLeuAlaLeuGlyThrLeuAlaPro 20
Db 44 ATGAAGTCCAGCGCCCTCTCCCTTCTGGTGTGCTGGCTGGGAATCTGGCACT 103
Qy 21 TrpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProProLysLysSer 40
Db 104 TGGGCTGTGGAAGGCTCTGGAAGTCTTCAAAGCTGGAGTCTGCTCTCTAAGAAATCT 163
Qy 41 AlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAspTyrGlnCysProGlyLys 60
Db 164 GCCCAGTGCCTTATGATACAAAGAACCTGAGTGCAGAGTGAATGCTGAGTGCAGGAAG 223
Qy 61 LysArgCysCysProAspThrCysGlyLysLysCysLeuAspProValAspThrProAsn 80
Db 224 AAGAGATGTTGCTCTGACACTTGTGGCATCAAATGCTGATGCTGTTGACACCCCAAC 283
Qy 81 ProThrArgArgLysProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAsn 100
Db 284 CCAACAAGGAGGAAGCTCGGAAGTGCAGTGCCTGATGCTATGGCCAATGTTGATGCTTAAC 343
Qy 101 ProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGly 120
Db 344 CCCCCCAATTCTGTGATGATGATGGCCAGTGCAGGCGTGAATGATGATGATGGGC 403
Qy 121 MetCysGlyLysSerCysValSerProValLysAla 132
Db 404 ATGTGTGGGAAATCTCGGTTATCCCTGTGGAAGCT 439

RESULT 6
BX089446
LOCUS
DEFINITION BX089446 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongseung@mail.kribb.re.kr

Plate: 31 row: E column: 12

High quality sequence stop: 597.

FEATURES

source
1. .597
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S14K402-31-E12"
/cell_line="K402"
/lab_hosts="Top10F"
/clone_lib="S14K402"
/notes="Organ: Stomach; Vector: pTZ19RP1; Site 1: EcoRI; Site 2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Alignment Scores:
Pred. No.: 3.79e-60 Length: 597
Score: 762.00 Matches: 132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-613-105-2 (1-132) x BM843274 (1-597)

Qy 1 MetLysSerSerGlyLeuPheProPheLeuValLeuAlaLeuGlyThrLeuAlaPro 20
Db 25 ATGAAGTCCAGCGGCTCTTCCGCTTCTGGTGTGCTGGCTGGGAACTCTGGCACCT 84
Qy 21 TrpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProProLysLysSer 40
Db 85 TGGGCTGTGGAAGGCTCTGGAAGTCTTCAAAGCTGGAGTCTGTCTCTTAAGAAATCT 144
Qy 41 AlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAspTrpGlnCysProGlyLys 60
Db 145 GCCAGTGCTTAGATACAGAAGAACTGAGTGCAGAGTACTGGCAGTGTCCAGGGAAG 204
Qy 61 LysArgCysCysProAspThrCysGlyLysLysCysLeuAspProValAspThrProAsn 80
Db 205 AAGAGATGTTGTCTGACACTTGTGGCATCAAAATGCTGGATCTGTGTGACACCCCAAC 264
Qy 81 ProThrArgArgLysProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAsn 100
Db 265 CCAACAAGGAGGAAGCCCTGGGAAGTGGCCAGTACTTATGGCAATGTTTGTGCTTAAC 324
Qy 101 ProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysMetGly 120
Db 325 CCCCCCAATTTCTGTGAGATGGATGGCCAGTGCACGCTGACTTGAAGTGTTCATGGGC 384
Qy 121 MetCysGlyLysSerCysValSerProValLysAla 132
Db 385 ATGTGTGGGAATCTCGCTTTCCTGTTGAAAGCT 420

RESULT 10

CD000587

LOCUS

599 bp mRNA linear EST 01-MAY-2003

DEFINITION

AGENCOURT_13648070 NIH_MGC_186 Homo sapiens cDNA clone

IMAGE:30323772 5', mRNA sequence.

CD000587

CD000587.1 GI:30295106

EST.

SOURCE

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 599)

NIH-MGC http://mgs.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

AUTHORS

Contact: Robert Straubeberg, Ph.D.

Email: cga@rs@mail.nih.gov

Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits

cDNA Library Preparation: CLONTECH Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: NDCM126 row: o column: 13

High quality sequence stop: 556.

FEATURES

source

1. .599
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30323772"
/lab_hosts="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 186"
/notes="Organ: Pooled-Skin; Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc); Site 2: SfiI (ggccctcgcc); Library is oligo-dT primed and directionally cloned cDNA was prepared from a pooled samples of tissues from Skin, meninges, duramater, pia matter and choroid plexus. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGGCGGCCACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.47 kb (range 0.50-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library"

ORIGIN

Alignment Scores:
Pred. No.: 3.8e-60 Length: 599
Score: 762.00 Matches: 132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-613-105-2 (1-132) x CD000587 (1-599)

Qy 1 MetLysSerSerGlyLeuPheProPheLeuValLeuAlaLeuGlyThrLeuAlaPro 20
Db 25 ATGAAGTCCAGCGGCTCTTCCGCTTCTGGTGTGCTGGCTGGGAACTCTGGCACCT 84
Qy 21 TrpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProProLysLysSer 40
Db 85 TGGGCTGTGGAAGGCTCTGGAAGTCTTCAAAGCTGGAGTCTGTCTCTTAAGAAATCT 144
Qy 41 AlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAspTrpGlnCysProGlyLys 60
Db 145 GCCAGTGCTTAGATACAGAAGAACTGAGTGCAGAGTACTGGCAGTGTCCAGGGAAG 204
Qy 61 LysArgCysCysProAspThrCysGlyLysLysCysLeuAspProValAspThrProAsn 80
Db 205 AAGAGATGTTGTCTGACACTTGTGGCATCAAAATGCTGGATCTGTGTGACACCCCAAC 264

priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli top10⁺ by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Alignment Scores: 3,86e-60 Length: 606
 Pred. No.: 762.00 Matches: 132
 Score: 100.00% Conservative: 0
 Percent Similarity: 100.00% Mismatches: 0
 Best Local Similarity: 100.00% Indels: 0
 Query Match: 100.00% Gaps: 0
 DB: 4

US-10-613-105-2 (1-132) x BM842052 (1-606)

QY 1 MetLysSerSerGlyLeuPheProPheLeuValLeuAlaLeuGlyThrLeuAlaPro 20
 DB 22 ATGAATTCAGCGGCTCTTCCCTTCTGGTCTGCTTCCCTGGGAACTCTGGCACCT 81
 QY 21 TtpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProLysLysSer 40
 DB 82 TGGGCTGTGGAGGCTCTGGAAAGTCTTCAAGCTGGAGTGTCTCTCTAAGAAATCT 141
 QY 41 AlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAspTrpGlnCysProGlyLys 60
 DB 142 GCCAGTGCCTTAGATACAGAAGCTGAGTGCAGAGTGACTGGCAGTGTCCAGGGAAG 201
 QY 61 LysArgCysProAspThrCysGlyLysCysLeuAspProValAspThrProAsn 80
 DB 202 AAGAGATGTCTGACACTTGTGCATCAAGTGCATGCTGATCTGTGTACACCCCAAC 261
 QY 81 ProThrArgArgLysProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAsn 100
 DB 262 CCACAAGGAGGAAGCTGGAGAGTGCACAGTACTTATGGCCAATGTTTGTATGCTTAAC 321
 QY 101 ProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGly 120
 DB 322 CCCCCCAATTTCTGTGAGATGGATGCCAGTGCAGCTGACTTGAAGTGTTCATGGGC 381
 QY 121 MetCysGlyLysSerCysValSerProValLysAla 132
 DB 382 ATGTGTGGGAATCTTCGCTTCCCTGTGGAAAGCT 417

RESULT 13

BM976429/c

LOCUS 612 bp mRNA linear EST 21-FEB-2003
 DEFINITION UI-CF-EN1-acz-n-15-0-UI.s1 UI-CF-EN1 Homo sapiens cDNA clone
 UI-CF-EN1-acz-n-15-0-UI 3', mRNA sequence.

ACCESSION BM976429

VERSION BM976429.1 GI:195994023

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS 1 (bases 1 to 612)

Bonaldi,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

JOURNAL MEDLINE 97044477

PUBMED 889548

COMMENT Contact: McCray, PB

McCrory Lab

University of Iowa

2024 University of Iowa Med Labs, Iowa City, IA 52242, USA

Tel: 319 356 4866

Fax: 319 356 7171
 Email: paul-mccray@uiowa.edu

Tissue Procurement: Dr. M. J. Welsh, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.regen.com) or from Open Biosystems
 (www.openbiosystems.com).
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES

source

1..612
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-CF-EN1-acz-n-15-0-UI"
 /tissue_type="Primary Lung Cystic Fibrosis Epithelial
 Cells"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /clone_lib="UI-CF-EN1"
 /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
 modified polylinker; Site_1: EcoR I; Site_2: Not I;
 following tissue(s): Primary Lung Cystic Fibrosis
 Epithelial Cells. The library was constructed according to
 Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
 1996. First strand cDNA synthesis was primed with an
 oligo-dT primer containing a Not I site. Double stranded
 cDNA was ligated to an EcoR I adaptor, digested with Not
 I, and cloned directionally into pT7T3-Pac vector. The
 oligonucleotide used to prime the synthesis of
 first-strand cDNA contains a library tag sequence that is
 located between the Not I site and the (dT)18 tail. The
 sequence tag for this library is CTGCTCAGGT.
 TAG_TISSUE=Human Lung Epithelial Cell lines untreated LPS
 6hr to LPS 24h
 TAG_LTB=UI-CF-EN1
 TAG_SEQ=CTGCTCAGGT"

ORIGIN

Alignment Scores: 3,91e-60 Length: 612
 Pred. No.: 762.00 Matches: 132
 Score: 100.00% Conservative: 0
 Percent Similarity: 100.00% Mismatches: 0
 Best Local Similarity: 100.00% Indels: 0
 Query Match: 100.00% Gaps: 0
 DB: 5

US-10-613-105-2 (1-132) x BM976429 (1-612)

QY 1 MetLysSerSerGlyLeuPheProPheLeuValLeuAlaLeuGlyThrLeuAlaPro 20
 DB 592 ATGAAGTCCAGCGGCTCTTCCCTTCTGGTCTGCTTCCCTGGGAACTCTGGCACCT 533
 QY 21 TtpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProLysLysSer 40
 DB 532 TGGGCTGTGGAGGCTCTGGAAAGTCTTCAAGCTGGAGTCTGTCTCTCTAAGAAATCT 473
 QY 41 AlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAspTrpGlnCysProGlyLys 60
 DB 472 GCCCAGTGCCTTAGATACAGAAGAACTGAGTGCAGAGTGACTGGCAGGGAAG 413
 QY 61 LysArgCysProAspThrCysGlyLysCysLeuAspProValAspThrProAsn 80
 DB 412 AAGAGATGTGTCTGACACTTGTGCATCAAAATGCTGATCTGTGTGACACCCCAAC 353
 QY 81 ProThrArgArgLysProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAsn 100
 DB 352 CCNACAGGAGGAGGAGCTGGGAGTGCACAGTACTTATGGCCCAATGTTGATGCTTAAC 293
 QY 101 ProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGly 120

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|||||
292 CCCCCCAATTCGTGAGATGGATGCCAGTGAAGCGTGACTTGAAGTGTTCATGGGC 233
|||||
121 MetCysGlySerCysValSerProValLysAla 132
|||||
232 ATGTGTGGGAATCCTGCGTTTCCCTGTGAAAGCT 197
|||||

RESULT 14
LOCUS BQ232871 626 bp mRNA linear EST 02-MAY-2002
DEFINITION AGENCOURT_7579635 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6057322
5', mRNA sequence.
ACCESSION BQ232871
VERSION BQ232871.1 GI:20414271
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 626)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLMI3320 row: j column: 11
High quality sequence stop: 546.
Location/Qualifiers
source 1..626
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6057322"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 68"
/notes="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.8 kb. Library constructed by Life
Technologies."

ORIGIN
Alignment Scores:
Pred. No.: 4,03e-60 Length: 626
Score: 762.00 Matches: 132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-10-613-105-2 (1-132) x BQ232871 (1-626)

QY 1 MetLysSerGlyLeuPheProPheLeuValLeuLeuAlaLeuGlyThrLeuAlaPro 20
|||||
DB 11 ATGAAGTCACGCGCCTCTTCCCTCTCGTGTGCTTGCCTGGGAACCTCTGGCACCT 70
|||||
QY 21 TPAlaValGlySerGlyLysSerPheLysAlaGlyValCysProProlLysLysSer 40
|||||
DB 71 TGGGCTGTGGAAGCCTCGAAGACCTTCAAGCTGGAGTCTGTCTCTCTAAGAAATCT 130
|||||
QY 41 AlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAspTrpGlnCysProGlyLys 60
|||||
DB 131 GCCCAGTGCCTTAGATACAGAAACCTAGTGCAGAGTACTGGCAGTGTCCAGGGAAG 190
|||||
QY 61 LysArgCysCysProAspThrCysGlyLysCysLeuAspProValAspThrProAsn 80
|||||

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Db 191 AAGAGATGTTGCTGCACACTTGTGGCATCAATGCTGGATCCTCTTGCACCCCAAC 250
QY 81 ProThrArgLysProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAsn 100
|||||
Db 251 CCACCAAGAGGAGAGCCTGGGAAGTCCCAAGTACTTATGGCCAAATGTTGATGCTTAAC 310
|||||
QY 101 ProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGly 120
|||||
Db 311 CCCCCCAATTCGTGAGATGGATGCCAGTGAAGCGTGACTTGAAGTGTTCATGGGC 370
|||||
QY 121 MetCysGlySerCysValSerProValLysAla 132
|||||
Db 371 ATGTGTGGGAATCCTGCGTTTCCCTGTGAAAGCT 406
|||||

RESULT 15
LOCUS CD103997 760 bp mRNA linear EST 15-MAY-2003
DEFINITION AGENCOURT_13980945 NIH_MGC_186 Homo sapiens cDNA clone
IMAGE:30371083 5', mRNA sequence.
ACCESSION CD103997
VERSION CD103997.1 GI:30757171
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 760)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM161 row: b column: 20
High quality sequence stop: 458.
Location/Qualifiers
source 1..760
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30371083"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: Pooled-Skin; Vector: pDNR-LIB; Site 1: SfiI
(ggcatattggcc); Site 2: SfiI (ggcgcttcggcc); Library is
oligo-dT primed and directionally cloned. cDNA was
prepared from a pooled samples of tissues from Skin,
meninges, duramater, pia matter and choroid plexus.
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGCGCGGCGCCGACATG-dt (30)BN-3',
(where B = A, C, G and N = A, C, G, or T). Average
insert size 1.47 kb (range 0.50-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
Library"

ORIGIN
Alignment Scores:
Pred. No.: 5.2e-60 Length: 760
Score: 762.00 Matches: 132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

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Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLCM2368 row: k column: 03
 High quality sequence stop: 605.

FEATURES

source
 1..906
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6209402"
 /tissue_type="ductal carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_110"
 /notes="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;
 Site 2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GCCACGAG(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
 Pred. No.: 1,896-59 Length: 906
 Score: 757.00 Matches: 131
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.34% Indels: 0
 DB: 5 Gaps: 0

US-10-613-105-2 (1-132) x BQ691723 (1-906)

QY 2 LysSerSerGlyLeuPheProPheLeuValLeuAlaLeuGlyThrLeuAlaProTIP 21
 DB 3 AAGTCCAGCGGCTCTTCCCTTCTGGTGTCTGCTGGCCCTGGAACTCTGGACCTGG 62
 QY 22 AlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProProLysLysSerAla 41
 DB 63 GCTGTGGAGGCTCTGGAAAGTCTCTCAAAGCTGGAGTGTCTCTCTTAAGAAATCTGCC 122
 QY 42 GluCysLeuArgTyrLysLysProGluCysGlnSerAspTrpGlnCysProGlyLysLys 61
 DB 123 CAGTGCTTAGATACAGAAACCTGAGTGCACAGTGACTGGCAGTGTCCAGGGAAG 182
 QY 62 ArgCysCysProAspThrCysGlyLysLysCysLeuAspProValAspThrProAsnPro 81
 DB 183 AGATGTGTCTGACACTTGTGGATCAATGCTGGATCTCTGTGACACCCCAACCCCA 242
 QY 82 ThrArgArgLysProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAsnPro 101
 DB 243 ACAAGGAGGAAGCTCTGGGAAGTGCACAGTGCATATATGGCAATGTTTGTATGCTTAACCCC 302
 QY 102 ProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGlyMet 121
 DB 303 CCCAATTTCTGTGAGATGGATGCCCAAGTGCACAGTGCACAGTGTGAAGTGTTCATGGGCATG 362
 QY 122 CysGlyLysSerCysValSerProValLysAla 132
 DB 363 TGTGGGAATCTCTGCGTTTCCCTGTGGAAGCT 395

RESULT 30

CD690425
 LOCUS
 DEFINITION
 EST6948 human nasopharynx Homo sapiens cDNA, mRNA sequence.
 EST690425
 ACCESSION
 CD690425.1 GI:32211162
 VERSION
 EST.
 KEYWORDS

SOURCE

ORGANISM
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS
 Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and
 Zeng,Y.-X.

TITLE

Transcriptional Gene Expression Profile of Human Nasopharynx

JOURNAL

COMMENT

Unpublished (2003)
 Contact: Yixin Zeng
 Cancer Center
 Sun Yat-sen University
 651 Dongfeng Road East, Guangzhou 510060, China
 Tel: 86-1380-9770-743
 Fax: 86-20-8775-4506
 Email: yxzeng@zeums.edu.cn.

FEATURES

source

1..541
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="normal nasopharynx"
 /clone_lib="human nasopharynx"
 /notes="ESTs generated from a normal nasopharynx cDNA
 library from southern Chinese"

ORIGIN

Alignment Scores:
 Pred. No.: 1,196-59 Length: 541
 Score: 756.00 Matches: 131
 Percent Similarity: 99.24% Conservatives: 0
 Best Local Similarity: 99.24% Mismatches: 1
 Query Match: 99.21% Indels: 0
 DB: 6 Gaps: 0

US-10-613-105-2 (1-132) x CD690425 (1-541)

QY 1 MetLysSerSerGlyLeuPheProPheLeuValLeuAlaLeuGlyThrLeuAlaPro 20
 DB 63 ATGAAGTCCAGCGGCTCTTCCCTTCTGGTGTCTGCTGGCCCTGGAACTCTGGCACCT 122
 QY 21 TtpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProProLysLysSer 40
 DB 123 TGGGCTGTGGGAAGGCTCTGGAAGTCTCTCAAAGCTGGAGTGTCTCTCTTAAGAAATCT 182
 QY 41 AlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAspTrpGlnCysProGlyLys 60
 DB 183 GCCCAGTGTCTTAGATACAGAAACCTGAGTGCACAGTGACTGGCAGTGTCCAGGGAAG 242
 QY 61 LysArgCysCysProAspThrCysGlyLysLysCysLeuAspProValAspThrProAsn 80
 DB 243 AACAGATGTGTCTGACACTTGTGGCATCAATGCTGGATCTCTGTGACACCCCAAC 302
 QY 81 ProThrArgArgLysProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAsn 100
 DB 303 CCAACAGGAGGAAGCTCTGGGAAGTGCACAGTGCATATATGGCAATGTTTGTATGCTTAAAC 362
 QY 101 ProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGly 120
 DB 363 CCCCCCAATTTCTGTGAGATGGATGCCCAAGTGCACAGTGCACAGTGTGAAGTGTTCATGGGC 422
 QY 121 MetCysGlyLysSerCysValSerProValLysAla 132
 DB 423 ATGTGTGGGAATCTCTGCGTTTCCCTGTGACAGCT 458

RESULT 31

AA572950
 LOCUS
 DEFINITION
 nm33a03.s1 NCI CGAP Lip2 Homo sapiens cDNA clone IMAGE:1061932
 similar to gb:R04470 ANTILEUKOPROTEINASE 1 (HUMAN);, mRNA sequence.
 AA572950
 ACCESSION
 AA572950.1 GI:2347478
 VERSION
 EST.
 KEYWORDS

```
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-x@mail.nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 448 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 437.
FEATURES
Location/Qualifiers
source
1. 582
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="liposarcoma"
/lab_host="DH10B"
/clone_lib="NCI CGAP Lip2"
/notes="Vector: pAMP10; mRNA made from liposarcoma. cDNA
made by oligo-dT priming. Non-directionally cloned.
Size-selected on agarose gel, average insert size 600 bp.
Reference: Krizman et al. (1996) Cancer Research
56:5380-5383."
ORIGIN
Alignment Scores:
Pred. No.: 1,31e-59 Length: 582
Score: 756.00 Matches: 131
Percent Similarity: 99.24% Conservative: 0
Best Local Similarity: 99.24% Mismatches: 1
Query Match: 99.21% Indels: 0
DB: 1 Gaps: 0
US-10-613-105-2 (1-132) x AA572950 (1-582)
QY 1 MetLysSerSerGlyLeuPheProPheLeuValLeuAlaLeuGlyThrLeuAlaPro 20
DB 9 ATGAAGTCCAGCGGCTCTTCCCTTACTGGTGTCTTGGCTTGGCTGGAACTCTGGCACT 68
QY 21 TrpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProProLysLysSer 40
DB 69 TGGGCTGTGGAAGCTCTGGAAGCTCTTCAAAGCTGGAGTCTGTCTCTCTAAGAAATCT 128
QY 41 AlaGlnCysLeuArgTyrlLysLysProGluCysGlnSerAspTrpGlnCysProGlyLys 60
DB 129 GCCCAGTGCCTTAGATACAAAGAACTCTGAGTGCAGAGTGAAGTGCAGGGAAG 188
QY 61 LysArgCysCysProAspThrCysGlyLysLysCysLeuAspProValAspThrProAsn 80
DB 189 AAGAGATGTTGCTTGACATCTTGGGATCAATGCTTGGATCTGTGTGACACCCCAAC 248
QY 81 ProThrArgArgLysProGlyLysCysProValThrTyrlGlnCysLeuMetLeuAsn 100
DB 249 CCAACAAGGAGGAAGCCCTGGGAAGTGCAGTGCCTTATGGCCAATGTTTGATGCTTAAC 308
QY 101 ProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGly 120
DB 309 CCCCCCAATTTCTGTAGATGGATGGCCAGTGAAGCGTGACTTGAAGTGTTCATGGGC 368
QY 121 MetCysGlyLysSerCysValSerProValLysAla 132
US-10-613-105-2 (1-132) x CD690400 (1-582)
QY 1 MetLysSerSerGlyLeuPheProPheLeuValLeuAlaLeuGlyThrLeuAlaPro 20
DB 62 ATGAAGTCCAGCGGCTCTTCCCTTCTGGTGTCTTGGCTTGGCTGGAACTCTGGCACT 121
QY 21 TrpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProProLysLysSer 40
DB 122 TGGGCTGTGGAAGCTCTGGAAGCTCTTCAAAGCTGGAGTCTGTCTCTCTAAGAAATCT 181
QY 41 AlaGlnCysLeuArgTyrlLysLysProGluCysGlnSerAspTrpGlnCysProGlyLys 60
DB 182 GCCCAGTGCCTTAGATACAAAGAACTCTGAGTGCAGAGTGAAGTGCAGGGAAG 241
QY 61 LysArgCysCysProAspThrCysGlyLysLysCysLeuAspProValAspThrProAsn 80
DB 242 AAGAGATGTTGCTTGACATCTTGGGATCAATGCTTGGATCTGTGTGACACCCCAAC 301
QY 81 ProThrArgArgLysProGlyLysCysProValThrTyrlGlnCysLeuMetLeuAsn 100
DB 302 CCAACAAGGAGGAAGCCCTGGGAAGTGCAGTGCCTTATGGCCAATGTTTGATGCTTAAC 361
QY 101 ProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGly 120
DB 362 CCCCCCAATTTCTGTAGATGGATGGCCAGTGAAGCGTGACTTGAAGTGTTCATGGGC 421
QY 121 MetCysGlyLysSerCysValSerProValLysAla 132
```



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Db      422 ATGTGTGGAAATCCTCGGTTTCCCTGTGAAGCT 457

RESULT 33
BU927919
LOCUS
DEFINITION BU927919 633 bp mRNA linear EST 18-OCT-2002
IMAGE:6653451 5', mRNA sequence.
ACCESSION BU927919
VERSION BU927919.1 GI:24116649
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 633)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-x@mail.nih.gov
Tissue Procurement: NCI
cDNA Library Preparation: Michael Brownstein Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM2903 row: i column: 03
High quality sequence stop: 553.
Location/Qualifiers
1. 633
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6653451"
/tissue_type="mixed (pool of 40 RNAs)"
/lab_host="DH10B (TI-phage-resistant)"
/clone_lib="NIH MGC 126"
/note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);
Site 2: SfiI (ggccgctcgcc); Double-stranded cDNA was
prepared from a pool of 40 cell line polyA+ RNAs (bladder
- 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -
4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,
kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell -
5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%,
salivary gland - 1.3%, and skin - 2.3%). 5' and 3'
adaptors were used in cloning as follows:
5'-AAGCAGTGTATCAACGACAGTGGCCATTACGCCGGG-3' and
5'-ATTTCAGAGCGGCGGCGGCATG-AT(30)NN-3'. Full-length
enriched library was constructed using the Clontech
Creator SMART kit and size-selected to contain the 0.5-1
kb size fraction (other fractions present in NIH_MGC_127
and NIH_MGC_128). Library created in the laboratory of T.
Udwin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH_MGC
Library."

FEATURES
source
ORIGIN
Alignment Scores:
Pred. No.: 2,23e-59 Length: 633
Score: 754.00 Matches: 131
Percent Similarity: 99.24% Conservative: 0
Best Local Similarity: 99.24% Mismatches: 1
Query Match: 98.95% Indels: 0
DB: 5 Gaps: 0

US-10-613-105-2 (1-132) x BU927919 (1-633)

Qy      1 MetLysSerSerGlyLeuPheProPheLeuValLeuAlaLeuGlyThrLeuAlaPro 20
Db      25 ATGAAGTCCACGCGCCCTTCCCTTCTGTGCTGCTTGCCTCGGAATCTGGCACT 84
Qy      21 TrpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProProLysLysSer 40

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Db      85 TGGGCTGTGGAAGGCTCTGGAAGTCTCTCAAGAGCTGGAGTGTCTCTCTCAAGAAATCT 144
Qy      41 AlaGlnCysLeuArgTyrIlysLysProGluCysGlnSerAspTrpGlnCysProGlyLys 60
145 GCCCAGTGCCTTATATACAGAAACCTGAGTGCAGAGTGCAGTGCAGTGCAGGGAAG 204
Qy      61 LysArgCysCysProAspThrCysGlyLysCysLeuAspProValAspThrProAsn 80
205 AAGAGATGTTGCTCTGACACTTGTGGCATAAATGCTGGATCCTGTTGACACCCCAAC 264
Qy      81 ProThrArgArgLysProGlyLysCysProValThrTyrGlnCysLeuMetLeuAsn 100
265 CCACCAAGGAGGAGGAGCTGGGAAGTGCACAGTGCATATATGCCCAATGTTGATGCTTAAC 324
Qy      101 ProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGly 120
325 CCCCCCAATTTCTGTGAGATGGATGCCAGTGCAGCGTGAAGTGAAGTGTTCATGGGC 384
Qy      121 MetCysGlyLysSerCysValSerProValLysAla 132
385 ATGTGTGGGAATCCTCGGTTTCCCTGTGAAGCT 420

RESULT 34
BM694343
LOCUS
DEFINITION BM694343 493 bp mRNA linear EST 28-FEB-2002
UI-E-C11-afp-h-21-0-UI.r1 UI-E-C11 Homo sapiens cDNA clone
UI-E-C11-afp-h-21-0-UI 5', mRNA sequence.
ACCESSION BM694343
VERSION BM694343.1 GI:19007601
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 493)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
JOURNAL 97044477
MEDLINE 889548
PUBMED
COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4155 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Reverse.
Location/Qualifiers
1. 493
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-C11-afp-h-21-0-UI"
/tissue_type="RPE and Choroid"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/note="Organ: eye; Vector: pRT3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-E-C11 is a normalized cDNA library containing the
following tissue(s): RPE and Choroid. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dr primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I

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adaptor, digested with Not I, and cloned directionally into p7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

ORIGIN

Alignment Scores:
 Pred. No.: 5,73e-59 Length: 493
 Score: 748.00 Matches: 129
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 98.16% Indels: 0
 DB: 4 Gaps: 0

US-10-613-105-2 (1-132) x BM694343 (1-493)

Qy 4 SerGlyLeuPheProPheLeuValLeuAlaLeuGlyThrLeuAlaProTTPAlaVal 23
 Db 3 AGCGGCTCTTCCCTTCCTGGTGTCTTCCCTGGAACTCTGGCACCTTGGCGTGTG 62
 Qy 24 GluGlySerGlyLysSerPheLysAlaGlyValCysProLysLysSerAlaGlnCys 43
 Db 63 GAAGGCTCTGGAAAGTCTTCNAAGCTGGAGTGTCTCTCTAAGAAATCTGCCAGTGC 122
 Qy 44 LeuArgTyrLysLysProGluCysGlnSerAspTTPGlnCysProGlyLysLysArgCys 63
 Db 123 CTTAGATACAGAAGCTGAGTGCAGAGTCACTGGCAGTGTCCAGGAGAGAGATGT 182
 Qy 64 CysProAspThrCysGlyLysLysCysLeuAspProValAspThrProAsnProThrArg 83
 Db 183 TGTCTCGACACTTGTGGCATCAATGCTGATCTCTTGCACCCCAACCAACAAAG 242
 Qy 84 ArgLysProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAsnProAsn 103
 Db 243 AGNAGGCTGGAAAGTGCAGTCACTATGGCCAAATGTTGATGCTTAACCCCAAT 302
 Qy 104 PheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGlyMetCysGly 123
 Db 303 TTCTGTGAGATGGATGCCAGTGCAGCGTCACTTGAAGTGTTCATGGGCATGTGTGG 362
 Qy 124 LysSerCysValSerProValLysAla 132
 Db 363 AAATCCTCGCTTCCCTGTGAAAGCT 389

RESULT 35

BM704851
 LOCUS
 DEFINITION UI-E-Cil-afp-h-21-0-UI.r2 UI-E-Cil Homo sapiens cDNA clone
 UI-E-Cil-afp-h-21-0-UI 5', mRNA sequence.

ACCESSION

BM704851

VERSION

BM704851.1 GI:19018109

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 567)
 Bonaldo,M.F., Lennon,G. and Soares,M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery

AUTHORS

Genome Res. 6 (9), 791-806 (1996)
 97044477
 MEDLINE
 PUBMED 8889548

COMMENT

Contact: Soares, MB
 Coordinated Laboratory for Computational Genomics
 University of Iowa
 375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565

FEATURES

source

1..567
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-E-Cil-afp-h-21-0-UI"
 /tissue_type="RPE and Choroid"
 /dev_stage="adult"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /clone_lib="UI-E-Cil"
 /note="Organ: eye; Vector: p7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-E-Cil is a normalized cDNA library containing the following tissue(s): RPE and Choroid. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor digested with Not I, and cloned directionally into p7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

ORIGIN

Alignment Scores:
 Pred. No.: 6,88e-59 Length: 567
 Score: 748.00 Matches: 129
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 98.16% Indels: 0
 DB: 4 Gaps: 0

US-10-613-105-2 (1-132) x BM704851 (1-567)

Qy 4 SerGlyLeuPheProPheLeuValLeuAlaLeuGlyThrLeuAlaProTTPAlaVal 23
 Db 3 AGCGGCTCTTCCCTTCCTGGTGTCTTCCCTGGAACTCTGGCACCTTGGCGTGTG 62
 Qy 24 GluGlySerGlyLysSerPheLysAlaGlyValCysProLysLysSerAlaGlnCys 43
 Db 63 GAAGGCTCTGGAAAGTCTTCNAAGCTGGAGTGTCTCTCTAAGAAATCTGCCAGTGC 122
 Qy 44 LeuArgTyrLysLysProGluCysGlnSerAspTTPGlnCysProGlyLysLysArgCys 63
 Db 123 CTTAGATACAGAAGCTGAGTGCAGAGTCACTGGCAGTGTCCAGGAGAGAGATGT 182
 Qy 64 CysProAspThrCysGlyLysLysCysLeuAspProValAspThrProAsnProThrArg 83
 Db 183 TGTCTCGACACTTGTGGCATCAATGCTGATCTCTTGCACCCCAACCAACAAAG 242
 Qy 84 ArgLysProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAsnProAsn 103
 Db 243 AGNAGGCTGGAAAGTGCAGTCACTATGGCCAAATGTTGATGCTTAACCCCAAT 302
 Qy 104 PheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGlyMetCysGly 123
 Db 303 TTCTGTGAGATGGATGCCAGTGCAGCGTCACTTGAAGTGTTCATGGGCATGTGTGG 362
 Qy 124 LysSerCysValSerProValLysAla 132
 Db 363 AAATCCTCGCTTCCCTGTGAAAGCT 389

Email: bento-soares@uiowa.edu
 Tissue Procurement: Dr. Gregg Hageman
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
 Seq primer: M13 Reverse.

```

RESULT 36
BI489624      962 bp      mRNA      linear      EST 28-AUG-2001
LOCUS        603032084F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5173293 5',
DEFINITION   mRNA sequence.
ACCESSION    BI489624
VERSION      BI489624.1 GI:15328852
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/
1 (bases 1 to 962)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Prepared by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1431 row: g column: 22
High quality sequence stop: 555.
FEATURES
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        1..962
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:5173293"
            /lab_host="DH10B"
            /clone_lib="NIH_MGC_115"
            /notes="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
sequence anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."
ORIGIN
Alignment Scores:
Pred. No.:      1.38e-58      Length:      962
Score:          748.00      Matches:    129
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:     98.16%      Indels:    0
DB:              4          Gaps:       0

US-10-613-105-2 (1-132) x BI489624 (1-962)

QY      4 SerGlyLeuPheProPheLeuValLeuAlaLeuGlyThrLeuAlaProTrpAlaVal 23
DB      18 AGCGGCGCTCTCCCTTCCTGGTGTCTGCTTGGCCCTGGGAACCTGGCACCTTGGGCTGTG 77
QY      24 GluGlySerGlyLysSerPheLeuAlaGlyValCysProProLysLysSerAlaGlnCys 43
DB      78 GAAGGCTCTGGAAGAGTCCTTCAAGCTGGAGTCTGTCTCTAAGAAATCTGCCAGTGC 137
QY      44 LeuArgTyrLysLysProGluCysGlnSerAspTrpGlnCysProGlyLysLysArgCys 63
DB      138 CTTAGATACAAAGAAACCTGAGTGCCAGAGTGACTGGCAGGTGTCCAGGGAAGAGAGATGT 197
QY      64 CysProAspThrCysGlyLysLysCysLeuAspProValAspThrProAsnProThrArg 83
DB      198 TGTCTTGACACTTGTGGCATCAATGCCTGGATCCTGTTGACACCCCAACCAAGG 257

QY      84 ArgLysProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAsnProProAsn 103
DB      258 AGGAAGCCTGGGAAGTCCAGTGACTTATGGCAATGTTGATGCTTAACCCCAAT 317
QY      104 PheCysGlyMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGlyMetCysGly 123
DB      318 TTCTGTGAGATGGATGGCCAGTCAAGCGTGAAGTGTTCATGGCATGTGGGG 377
QY      124 LysSerCysValSerProValLysAla 132
DB      378 AAATCCTGGTTCCTCCCTGTGAAGCT 404

RESULT 37
AW264225/c
LOCUS        AW264225
DEFINITION   similar to gb:X04470 ANTILEUKOPROTEINASE 1 (HUMAN), mRNA sequence.
ACCESSION    AW264225
VERSION      AW264225.1 GI:6641126
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 575)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGAAP), Tumor Gene Index
Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Possible reversed clone: polyT not found
Seq primer: -400P from Gibco
High quality sequence stop: 411.
FEATURES
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        1..575
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            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:2758762"
            /tissue_type="three pooled meningiomas"
            /lab_host="DH10B"
            /clone_lib="NCI_CGAP_Brn53"
            /notes="Organ: brain; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies."
ORIGIN
Alignment Scores:
Pred. No.:      8.67e-59      Length:      575
Score:          747.00      Matches:    129
Percent Similarity: 98.47%      Conservative: 0
Best Local Similarity: 98.47%      Mismatches: 2
Query Match:     98.03%      Indels:    0
DB:              2          Gaps:       0

US-10-613-105-2 (1-132) x AW264225 (1-575)

QY      2 LysSerSerGlyLeuPheProPheLeuValLeuAlaLeuGlyThrLeuAlaProTrp 21
DB      573 AAGTCACCGCGCTTCTTCCCTTCCTGGTGTCTGCTTGGGGAACCTCTGGCACCTTGG 514

```

QY 22 AlavalGluGlySerGlyLysSerPheLysAlaGlyValCysProProLysLysSerAla 41
 |||||
 Db 513 GCTGTGGAGGCTCTGGAAGTCTTCAAGCTGGAGTCTGCTCTCTAGAAATCTGCC 454
 |||||
 QY 42 GlnCysLeuArgTyrLysLysProGluCysGlnSerAspTrpGlnCysProGlyLysLys 61
 |||||
 Db 453 CAGTGCCTTAGATACAAAGAAACCTGAGTGCAGAGTCTGAGTGCAGAGTCTGAGTGCAGGAGAAAG 394
 |||||
 QY 62 ArgCysCysProAspThrCysGlyLysLysCysLeuAspProValAspThrProAsnPro 81
 |||||
 Db 393 AGATGTGTCTGACACTTGGGATCAAAATGCTGGATCTGTGTGACACCCCAACCCA 334
 |||||
 QY 82 ThrArgArgLysProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAsnPro 101
 |||||
 Db 333 ACAGGAGGAGGCTGGGAGTGCAGTCTATGCGCCCAATGTTGATGCTTAACCCC 274
 |||||
 QY 102 ProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGlyMet 121
 |||||
 Db 273 CCCAATTTCTGTGAGATGGATGGCAGTGCAGGCTGACITGAAGTGTTCATGGGCATG 214
 |||||
 QY 122 CysGlyLysSerCysValSerProValLysAla 132
 |||||
 Db 213 TGTGGGAAATCTCTGCTTCCCTGTGAAAGCT 181
 |||||
 RESULT 38
 CBI51317 580 bp mRNA linear EST 29-JAN-2003
 LOCUS K-EST0208192 C1SNUI7 Homo sapiens cDNA clone C1SNUI7-28-C11 5',
 DEFINITION mRNA sequence.
 CBI51317
 CBI51317.1 GI:28135601
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.
 TITLE 21C Frontier Korean EST Project 2001
 JOURNAL Unpublished (2002)
 COMMENT Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongseung@mail.kribb.re.kr
 Plate: 28 row: C column: 11
 High quality sequence stop: 580.
 FEATURES
 source Location/Qualifiers
 1..580
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="C1SNUI7-28-C11"
 /sex="F"
 /tissue_type="Uterine"
 /cell_type="Epithelial"
 /cell_line="GNU-17"
 /lab_host="Top10P"
 /clone_lib="C1SNUI7"
 /note="Organ: Cervix; Vector: pCNS-D2; Site 1: EcoRI;
 Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
 bacterial alkaline phosphatase (BAP) and then decapped
 with tabacco acid pyrophosphatase (TAP). The decapped
 intact mRNA was ligated with DNA-RNA linker including
 EcoRI site by treatment of T4 RNA ligase and the first
 strand cDNA was synthesized from oligo dt-selected mRNA by
 priming with dt-tailed vector. The dt-tailed vector was
 adjusted to have about 60nt. The cDNA vector was
 circularized with E. coli DNA ligase after digestion of

ECORI which site is also included in vector. An RNA strand
 converted to a DNA strand by Okayama-Berg method. The
 obtained cDNA vectors were used for transformation of
 competent cells E. coli Top10P' by electroporation method.
 The cDNA libraries constructed by this method are
 full-length enriched cDNA library."

ORIGIN

Alignment Scores: 1,08e-58 Length: 580
 Pred. No.: 746.00 Matches: 130
 Score: 746.00
 Percent Similarity: 98.48% Conservative: 0
 Best Local Similarity: 98.48% Mismatches: 2
 Query Match: 97.90% Indels: 0
 DB: 6 Gaps: 0

US-10-613-105-2 (1-132) x CBI51317 (1-580)

QY 1 MetLysSerSerGlyLeuPheProPheLeuValLeuAlaLeuGlyThrLeuAlaPro 20
 |||||
 Db 37 ATGAAGTCCAGCGGCTCTTCCCTTCTGCTGCTGCTGGGAACTCTGGCACCT 96
 |||||
 QY 21 TrpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProProLysLysSer 40
 |||||
 Db 97 TGGGCTGTGGAGGCTCTGAAAAGTCTTCAAAAGCTGGAGTCTGCTCTCTATAAATCT 156
 |||||
 QY 41 AlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAspTrpGlnCysProGlyLys 60
 |||||
 Db 157 GCCCAGTGCTTAGATACAAAGAACTGAGTGCAGAGTACTGGCAGGTGTCACGGGAAG 216
 |||||
 QY 61 LysArgCysCysProAspThrCysGlyLysLysCysLeuAspProValAspThrProAsn 80
 |||||
 Db 217 AGAGATGTTACCCGACACTTGTGGCATCAATGCTGGATCTGTGACACCCCAAC 276
 |||||
 QY 81 ProThrArgArgLysProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAsn 100
 |||||
 Db 277 CCAACAAGAGGAGGAGCTGGGAAGTCCGAGTACTATGGCCAATGTTTGTATGCTTAAC 336
 |||||
 QY 101 ProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGly 120
 |||||
 Db 337 CCCCCCAATTTCTGTGAGATGGATGCCAGTGCAGGCTGACCTTGATGTTGCAATGGGC 396
 |||||
 QY 121 MetCysGlyLysSerCysValSerProValLysAla 132
 |||||
 Db 397 ATGTGTGGGAATCTCTGCTTCCCTGTGAAAGCT 432
 |||||
 RESULT 39
 BE396187 483 bp mRNA linear EST 21-JUL-2000
 LOCUS 601308817F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3626789 5',
 DEFINITION mRNA sequence.
 BE396187
 BE396187.1 GI:9341552
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: ARCC
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLCW309 row: b column: 06
 High quality sequence start: 5

High quality sequence stop: 481.
 FEATURES
 source
 1. 483
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3625394"
 /tissue_type="endometrium, adenocarcinoma cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_44"
 /notes="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN
 Alignment Scores:
 Pred. No.: 3,04e-58 Length: 483
 Score: 740.00 Matches: 128
 Percent Similarity: 98.46% Conservative: 0
 Best Local Similarity: 98.46% Mismatches: 2
 Query Match: 97.11% Indels: 0
 DB: 2 Gaps: 0

US-10-613-105-2 (1-132) x BE396187 (1-483)

QY 3 SerSerGlyLeuPheProPheLeuValLeuAlaLeuGlyThrLeuAlaProTrpAla 22
 DB 34 AGTCAGCGGCTCTTCCCTTCTCGTGTCTGCTGGCAACTCTGGCACCTTGGGCT 93

QY 23 ValGluGlySerGlyLysSerPheLysAlaGlyValCysProLysLysSerAlaGln 42
 DB 94 GTGGAAGGCTCTGGAAGTCTTCAAGCTGGAGTCTGCTCTTGAAGAAATCTGCCAG 153

QY 43 CysLeuArgTyrLysLysProGluCysGlnSerAspTrpGlnCysProGlyLysLysArg 62
 DB 154 TGCCTTAGATACAGAAACCTGAGTGCACAGTGACTGGCAGTGTCCAGGGAAGAAGA 213

QY 63 CysCysProAspThrCysGlyLysCysLeuAspProValAspThrProAsnProThr 82
 DB 214 TGTTCCTGACACTTGTGGCATCAATGCTGGATCTCTTGGACACCCCAACCA 273

QY 83 ArgArgLysProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAsnProPro 102
 DB 274 AGAGGAAGCTGGGAAGTGCACAGTGACTTATGGCCAAATGTTGATGCTTAACCCCCC 333

QY 103 AsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGlyMetCys 122
 DB 334 AATTCTGTGAGATGGATGCCAGTGCACGGTGACTTGAAGTGTTCATGGGCATGTGT 393

QY 123 GlyLysSerCysValSerProValLysAla 132
 DB 394 GGGAAATCTCTGCGTTTCCCTGTGAAAGCT 423

RESULT 40
 BE392080 581 bp mRNA linear EST 21-JUL-2000
 LOCUS 601307712F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3625394 5',
 DEFINITION mRNA sequence.
 BE392080
 BE392080.1 GI:9337445
 EST.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 581)
 NIH-MGC http://mgi.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL

Contact: Robert Straubeberg, Ph.D.
 Email: cgaabs-i@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLC305 row: h column: 03
 High quality sequence start: 4
 High quality sequence stop: 560.
 Location/Qualifiers
 1. 581
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3625394"
 /tissue_type="endometrium, adenocarcinoma cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_44"
 /notes="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN
 Alignment Scores:
 Pred. No.: 5.92e-58 Length: 581
 Score: 738.00 Matches: 127
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 96.85% Indels: 0
 DB: 2 Gaps: 0

US-10-613-105-2 (1-132) x BE392080 (1-581)

QY 6 LeuPheProPheLeuValLeuLeuAlaLeuGlyThrLeuAlaProTrpAlaValGluGly 25
 DB 1 CTCTTCCCTTCTCGTGTCTGCTGGCAACTCTGGCACCTTGGGCTTGGGAAGGC 60

QY 26 SerGlyLysSerPheLysAlaGlyValCysProLysLysSerAlaGlnCysLeuArg 45
 DB 61 TCTGGAAGTCTTCAAGCTGGAGTCTGCTCTTGAAGAAATCTGCCAGTGCCTTAGA 120

QY 46 TyrLysLysProGluCysGlnSerAspTrpGlnCysProGlyLysLysArgCysCysPro 65
 DB 121 TACAAGAAACCTGAGTGCACAGTGTGTCAGTGTCCAGGGAAGAAGAGATGTGTCT 180

QY 66 AspThrCysGlyLysCysLeuAspProValAspThrProAsnProThrArgArgLys 85
 DB 181 GACACTTGTGGCATCAATGCTGGATCTTGTGACACCCCAACCAAGAGAGAG 240

QY 86 ProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAsnProProAsnPheCys 105
 DB 241 CTGGGAAGTGCACAGTGTATGGCAATGTTGATGCTTAACCCCAATTTCTGT 300

QY 106 GluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGlyMetCysGlyLysSer 125
 DB 301 GAGATGGATGGCCAGTCAAGCGTGAAGTGTTCATGGGCATGTGTGGGAATCC 360

QY 126 CysValSerProValLysAla 132
 DB 361 TGCCTTCCCTGTGAAAGCT 381

RESULT 41
 BE743613 557 bp mRNA linear EST 15-SEP-2000
 LOCUS 601573751F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834636 5',
 DEFINITION mRNA sequence.

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ACCESSION BE743613
VERSION BE743613.1 GI:10157605
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 557)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCMS15 row: f column: 13
High quality sequence stop: 557.
Location/Qualifiers
FEATURES
source
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3834636"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_9"
/notes="Organ: Ovary; Vector: pOT87; Site:1: XhoI; Site:2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

Alignment Scores: 1.31e-57 Length: 557
Pred. No.: 734.00 Matches: 126
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 96.33% Gaps: 2
DB: 2

US-10-613-105-2 (1-132) x BE743613 (1-557)

Qy 7 PheProPheLeuValLeuLeuAlaLeuGlyThrLeuAlaProTTPAlaValGluGlySer 26
Db 2 TTCCCTTCTCTGGTGTCTTGGCTGGGAACTCTGGCACCTTGGGCTGTGGAGGCTCT 61

Qy 27 GlyLysSerPheLysAlaGlyValCysProProLysLysSerAlaGlnCysLeuArgTyr 46
Db 62 GGAAGTCCCTTCAAGAGTGGAGTCTGTCTCTCTAAGAAATCTGCCAGTGCCTTAGATAC 121

Qy 47 LysLysProGluCysGlnSerAspTTPGlnCysProGlyLysLysArgCysCysProAsp 66
Db 122 AAGAAACCTGAGTGCCAGAGTGAATGGCAGTGTCCAGGGAAGAAGAGATGTTGCTCTGAC 181

Qy 67 ThrCysGlyLysLysCysLeuAspProValAspThrProAsnProThrArgArgLysPro 86
Db 182 ACTTGTGGCATCAATGCCCTGGATTCCTTTGTACACCCCAACCCCAACAGAGAGACCT 241

Qy 87 GlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAsnProProAsnPheCysGlu 106
Db 242 GGAAGTGCCTGAGTGAATGTCCTTATGGCAATGTTGATGCTTAACCCCAATTTCTGTGAG 301

Qy 107 MetAspGlyGlnCysLysArgAspLeuLysCysCysMetGlyMetCysGlyLysSerCys 126
Db 302 ATGGATGGCCAGTGCAAGCGTGAATTTGAAGTGTGTCATGGGCATGTGTGGGAAATCCTGC 361

Qy 127 ValSerProValLysAla 132
Db 362 GTTTCCTCTGTGAAGCT 379

RESULT 42
BI819626
LOCUS BI819626
DEFINITION 603034162F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5175327 5',
mRNA sequence.
ACCESSION BI819626 583 bp mRNA linear EST 04-OCT-2001
VERSION BI819626.1 GI:15931176
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 583)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11436 row: 1 column: 16
High quality sequence stop: 562.

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5175327"
/lab_host="DH10B"
/clone_lib="NIH_MGC_115"
/notes="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site:1: NotI; Site:2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."

Alignment Scores: 1.39e-57 Length: 583
Pred. No.: 734.00 Matches: 126
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 96.33% Gaps: 4
DB: 4

US-10-613-105-2 (1-132) x BI819626 (1-583)

Qy 7 PheProPheLeuValLeuLeuAlaLeuGlyThrLeuAlaProTTPAlaValGluGlySer 26
Db 2 TTCCCTTCTCTGGTGTCTTGGCTGGGAACTCTGGCACCTTGGGCTGTGGAGGCTCT 61

Qy 27 GlyLysSerPheLysAlaGlyValCysProProLysLysSerAlaGlnCysLeuArgTyr 46
Db 62 GGAAGTCCCTTCAAGAGTGGAGTGTCTCTCTCTAAGAAATCTGCCAGTGCCTTAGATAC 121

Qy 47 LysLysProGluCysGlnSerAspTTPGlnCysProGlyLysLysArgCysCysProAsp 66
Db 122 AAGAAACCTGAGTGCCAGAGTGAATGGCAGTGTCCAGGGAAGAAGAGATGTTGCTCTGAC 181

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QY 67 ThrCysGlyLeuLysCysLeuAspProValAspThrProAsnProThrArgArgLysPro 86
DB 182 ACTTGTGGCATCAATAGCTGGATCTGTTGACACCCCAACCAAGGAGGAAAGCCT 241
QY 87 GlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAsnProProAsnPhCysGlu 106
DB 242 GGAAGTGGCCAGTGAATGATGCGCAATGTTGATGCTTAACCCCCCAATTTCTGTGAG 301
QY 107 MetAspGlyGlnCysLysArgAspLeuLysCysMetGlyMetCysGlyLysSerCys 126
DB 302 ATGGATGGCCAGTGCAGGCGTGAATGAGTGTGATGGCATGTGTGGGAATCTCTGC 361
QY 127 ValSerProValLysAla 132
DB 362 GTTTCCTGCTGAAAGCT 379

RESULT 43
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LOCUS
DEFINITION
602505842F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4619099 5',
mRNA sequence.
ACCESSION
BG484664
VERSION
BG484664.1 GI:13416943
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 770)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1378 row: d column: 12
High quality sequence stop: 554.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_77"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggcgctcgcc); Site 2: SfiI (ggcattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCCCGCGCCGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

FEATURES
source
1..770
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_77"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggcgctcgcc); Site 2: SfiI (ggcattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCCCGCGCCGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores: 2.47e-57 Length: 770
Pred. No.: 733.00 Matches: 131
Score: 99.24% Conservative: 0
Percent Similarity: 99.24% Mismatches: 1
Best Local Similarity: 96.19% Indels: 1
Query Match: 4 Gaps: 0
DB: 4

US-10-613-105-2 (1-132) x BG484664 (1-770)

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QY 1 MetLysSerSerGlyLeuPhePheProPheLeuValLeuAlaLeuGlyThrLeuAlaPro 20
DB 23 ATGAAGTCAGCGGCCTCTTCCCTTCTGGTGTCTCTTCCCTGGCAACTCTGGCACT 82
QY 21 TrpAlaValIleGlySerGlyLysSerPheLysAlaGlyValCysProPolysLysSer 40
DB 83 TGGGCTGTGGAGGGCTCTGGAAAGTCTTCAAAGCTGGAGTCTGTCTCTCTAAGAAATCT 142
QY 41 AlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAspTrpGlnCysProGlyLys 60
DB 143 GCCCAGTGGCTTAGATACAGAAACCTGAGTGCACAGTGACTGGCAGTGTCCAGGGAAG 202
QY 61 LysArgCysCysProAspThrCysGlyLysLeuLysCysLeuAspProValAspThrProAsn 80
DB 203 AAGAGATGTTGTCTGACACTTGTGGCATCAATGGCTGGATCTCTGTGTGACACCCAAA - 261
QY 81 ProThrArgArgLysProGlyLysCysProValThrTyrGlyGlnCysValLeuMetLeuAsn 100
DB 262 CCAACAGGAGGAGGAGGCTGGGAAGTCCCGAGTGACTTATGGCAATGTTTGTATGCTTAAAC 321
QY 101 ProProAsnPhCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGly 120
DB 322 CCCCCCAATTTCTGTGAGATGGATGCCAGTGCAAGCGTGACTTGAAGTGTTCATGGGC 381
QY 121 MetCysGlyLysSerCysValSerProValLysAla 132
DB 382 ATGTGTGGAAATCTCGCTTCCCTGTGAAAGCT 417

RESULT 44
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LOCUS
DEFINITION
601140427F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049710 5',
mRNA sequence.
ACCESSION
BE271401
VERSION
BE271401.1 GI:9145136
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 793)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM94 row: e column: 07
High quality sequence stop: 577.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="IMAGE:3049710"
/lab_host="DH10B (phage-resistant)"
/issue_type="adenocarcinoma cell line"
/clone_lib="NIH_MGC_9"
/note="Organ: ovary; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

```

Alignment Scores:

Pred. No.: 7,42e-57 Length: 793
 Score: 726.00 Matches: 125
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 95.54% Indels: 0
 DB: 2 Gaps: 0

US-10-613-105-2 (1-132) x BE271401 (1-793)

QY 8 PropheLeuValLeuLeuAlaLeuGlyThrLeuAlaProTrpAlaValGluGlySerGly 27
 Db 2 CCCTTCTGGTGTCTGTCCTTGGAACTCTGGCACCCTGGGCTGTGGAAGCTCTGGA 61
 QY 28 LysSerPheLysAlaGlyValCysProProLysLysSerAlaGlnCysLeuArgTyrLys 47
 Db 62 AAGTCCTTCAAGCTGAGTCTGCTCTCTAAGAAATCTGCCAGTGCCTTAGATACAAG 121
 QY 48 LysProGluCysGlnSerAspTrpGlnCysProGlyLysLysArgCysCysProAspThr 67
 Db 122 AAACCTGAGTGCAGAGTACTGGCAGTGTCCAGGAAGAGAGATGTTGTCTTGACACT 191
 QY 68 CysGlyLysCysLeuAspProValAspThrProAsnProThrArgArgLysProGly 87
 Db 182 TGTGGCATCAAAATGCCTGGATCTGTTGACACCCCAACCAAGAGGAGGAGCCTGGG 241
 QY 88 LysCysProValThrTyrGlnCysLeuMetLeuAsnProProAsnPheCysGluMet 107
 Db 242 AAGTGCCAGTGACTTATGCGCAATGTTTGATGCTTAACCCCCCAATTTCTGTGAGATG 301
 QY 108 AspGlyGlnCysLysArgAspLeuLysCysCysMetGlyMetCysGlyLysSerCysVal 127
 Db 302 GATGGCCAGTGCAAGCGTGACTTGAAGTGTTCATGGCATGGGCAATGCTCGGTT 361
 QY 128 SerProValLysAla 132
 Db 362 TCCCTGTGAAGCT 376

RESULT 45

CD699640 511 bp mRNA linear EST 25-JUN-2003
 LOCUS EST16036 human nasopharynx Homo sapiens cDNA, mRNA sequence.
 DEFINITION CD699640
 ACCESSION CD699640
 VERSION CD699640.1 GI:32228866
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 511)
 Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and
 Zeng,Y.-X.
 TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
 JOURNAL Unpublished (2003)
 COMMENT Contact: Yixin Zeng
 Cancer Center
 Sun Yat-sen University
 651 Dongfeng Road East, Guangzhou 510060, China
 Tel: 86-1380-9770-743
 Fax: 86-20-8775-4506
 Email: yxzeng@zeums.edu.cn.

FEATURES

source
 1..511
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue type="normal nasopharynx"
 /clone_lib="human nasopharynx"
 /notes="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

ORIGIN

Alignment Scores:

Pred. No.: 6,37e-57 Length: 511
 Score: 726.00 Matches: 130
 Percent Similarity: 97.74% Conservatives: 0
 Best Local Similarity: 97.74% Mismatches: 2
 Query Match: 95.28% Indels: 1
 DB: 6 Gaps: 0

US-10-613-105-2 (1-132) x CD699640 (1-511)

QY 1 MetLysSerSerGlyLeuPheProPheLeuValLeuAlaLeuGlyThrLeuAlaPro 20
 Db 44 ATGAAGTCCAGCGGCTCTTCCCTTCTCTGGTGTCTCTTGGCCCTGGGAACCTCTGGCACCT 103
 QY 21 Trp-AlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProProLysLysSe 40
 Db 104 TGTGGCTGTGGAAGGCTCTGSAAGTCTTCAAAAGCTGGAGTCTGTCTCTTAAGAAATC 163
 QY 40 xAlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAspTrpGlnCysProGlyLy 60
 Db 164 TGCCCAAGTCCCTTAGATACAAGAACTGAGTGCCAGAGTGAAGTGGCAGTGTCCAGGAA 223
 QY 60 sLysArgCysCysProAspThrCysGlyLysLysCysLeuAspProValAspThrProAs 80
 Db 224 GAAGAGATGTTGTCTGACACTTGTGGCATCAAAATGCCTGGATCTCTGTGTGACACCCCAA 283
 QY 80 nProThrArgArgLysProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAs 100
 Db 284 CCCAACAGGAGGAAGCCTGGGAAGTGGCCAGTGAATATGGCCAAATGTTGATGCTTAA 343
 QY 100 nProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysMetGl 120
 Db 344 CCCCCCAATTTCTGTGAGATGGATGGCCAGTGGCAAGCGTGACTTGAAAGTGTAGCATGGG 403
 QY 120 yMetCysGlyLysSerCysValSerProValLysAla 132
 Db 404 CATGTGTGGAAATCCTGCGTATCCCTGTGAAAGCT 440

Search completed: October 24, 2004, 05:52:24

Job time : 2736 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: October 24, 2004, 04:00:14 ; Search time 427 Seconds
(without alignments)
1583.976 Million cell updates/sec

Title: US-10-613-105-2

Perfect score: 762

Sequence: 1 MKSSGLFPFLVLLALGLTAP.....RDLKCCMGCMGKSCVSPVKA 132

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Xgapop 10.0 , Xgapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3407233 seqs, 2561960514 residues

Total number of hits satisfying chosen parameters: 6814466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Command line parameters:

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-DB=Published Applications NA -Qfmt=fastap -SUFFIX=rnpb -MINWATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=100 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=45 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10613105 @CGN 1.1 480 @runat_22102004_170442_18724
-NCPU=6 -ICPU=3 -NO MAP -LARGQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-XGAPOP=6 -XGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA:
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4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
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10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
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16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

*

Result No.	Score	Query Match	Length	DB	ID	Description
1	762	100.0	399	15	US-10-257-021-53	Sequence 53, Appl
2	762	100.0	399	15	US-10-172-118-864	Sequence 864, App
3	762	100.0	399	16	US-10-342-887-864	Sequence 864, App
4	762	100.0	422	16	US-10-309-290-141	Sequence 141, App
5	762	100.0	565	15	US-10-360-368-1	Sequence 1, Appl
6	762	100.0	594	9	US-09-964-824A-582	Sequence 582, App
7	762	100.0	594	9	US-09-954-456-1989	Sequence 1989, App
8	762	100.0	594	9	US-09-865-812-1	Sequence 1, Appl
9	762	100.0	594	14	US-10-097-340-295	Sequence 295, App
10	762	100.0	594	15	US-10-205-823-374	Sequence 374, App
11	762	100.0	594	15	US-10-172-293-429	Sequence 429, App
12	762	100.0	594	15	US-10-172-118-863	Sequence 863, App
13	762	100.0	594	16	US-10-305-720-1271	Sequence 1271, App
14	762	100.0	594	16	US-10-309-290-143	Sequence 143, App
15	762	100.0	594	16	US-10-240-425-1529	Sequence 1529, App
16	762	100.0	594	16	US-10-342-887-863	Sequence 863, App
17	762	100.0	594	17	US-10-613-105-1	Sequence 1, Appl
18	762	100.0	594	17	US-10-322-696-123	Sequence 123, App
19	762	100.0	598	15	US-10-177-293-431	Sequence 431, App
20	762	100.0	598	16	US-10-173-999-153	Sequence 153, App
21	762	100.0	1084	10	US-09-814-353-20587	Sequence 20587, A
22	638.5	83.8	1525	14	US-10-025-514-15	Sequence 15, Appl
23	635	83.3	321	14	US-10-025-514-3	Sequence 3, Appl
24	635	83.3	321	16	US-10-309-290-145	Sequence 145, App
25	635	83.3	1525	14	US-10-025-514-7	Sequence 7, Appl
26	537.5	70.5	22324	17	US-10-322-696-124	Sequence 124, App
27	463.5	60.8	1079	17	US-10-322-696-122	Sequence 122, App
28	458	60.1	325	16	US-10-305-720-1024	Sequence 1024, App
29	352.5	46.3	422	15	US-10-125-159-37	Sequence 37, Appl
30	339	44.5	805	14	US-10-116-802-431	Sequence 431, App
31	285	37.4	4090	14	US-10-076-816-57	Sequence 57, Appl
32	283.5	37.2	313	10	US-09-814-353-2826	Sequence 2826, App
33	283.5	37.2	313	10	US-09-814-353-9156	Sequence 9156, App
34	277.5	36.4	38692	17	US-10-322-696-121	Sequence 121, App
C 35	264	34.6	411	9	US-09-964-824A-495	Sequence 495, App
C 36	264	34.6	411	9	US-09-954-456-1987	Sequence 1987, App
C 37	264	34.6	411	9	US-09-967-768A-3	Sequence 3, Appl
C 38	264	34.6	411	10	US-09-960-708-16	Sequence 16, Appl
C 39	264	34.6	411	10	US-09-873-319-9	Sequence 9, Appl
40	257.5	33.8	248	17	US-10-430-201-2236	Sequence 2236, App
41	257.5	33.8	248	17	US-10-430-201-2237	Sequence 2237, App
42	243	31.9	188	10	US-09-814-353-15540	Sequence 15540, A
43	232.5	30.5	518	15	US-10-125-159-43	Sequence 43, Appl
44	230	30.2	208	15	US-10-125-159-41	Sequence 41, Appl
45	224	29.4	232	9	US-09-884-441-377	Sequence 377, App
46	224	29.4	232	10	US-09-907-969-377	Sequence 377, App
47	224	29.4	232	10	US-09-827-271-377	Sequence 377, App
48	224	29.4	232	15	US-10-198-053-377	Sequence 14, Appl
49	212	27.8	732	15	US-10-221-097-14	Sequence 14, Appl
50	207	27.2	558	15	US-10-221-097-15	Sequence 15, Appl
51	185.5	24.3	1010	17	US-10-729-807-27	Sequence 27, Appl
52	185.5	24.3	1055	16	US-10-250-959-1	Sequence 1, Appl
53	165.5	21.7	374	15	US-10-233-150-12	Sequence 12, Appl
54	165.5	21.7	390	15	US-10-233-150-3	Sequence 3, Appl
55	165.5	21.7	486	15	US-10-233-150-10	Sequence 10, Appl
56	165.5	21.7	622	9	US-09-925-300-421	Sequence 421, App
57	165.5	21.7	622	16	US-10-264-049-627	Sequence 627, App
58	165.5	21.7	643	10	US-09-992-600A-41	Sequence 41, Appl
59	165.5	21.7	643	10	US-09-924-340-41	Sequence 41, Appl
60	165.5	21.7	643	10	US-09-992-095B-41	Sequence 41, Appl
61	165.5	21.7	643	10	US-09-999-570-41	Sequence 41, Appl
62	165.5	21.7	643	14	US-10-000-489-41	Sequence 41, Appl
63	165.5	21.7	643	14	US-10-000-986-41	Sequence 41, Appl
64	165.5	21.7	643	15	US-10-154-678-41	Sequence 41, Appl
65	165.5	21.7	643	15	US-10-001-142-41	Sequence 41, Appl
66	165.5	21.7	656	14	US-10-198-846-11505	Sequence 11505, A
67	165.5	21.7	1004	16	US-10-264-049-628	Sequence 628, App
68	165.5	21.7	1077	15	US-10-233-150-4	Sequence 4, Appl
69	165.5	21.7	1098	15	US-10-233-150-6	Sequence 6, Appl
70	163	21.4	584	15	US-10-295-027-501	Sequence 501, App


```
QY 1 MetLysSerSerGlyLeuPheProPheLeuValLeuLeuAlaLeuGlyThrLeuAlaPro 20
DB 19 ATGAAGTCCAGCGGCTCTTCCCTTCTGGTGTCTGCTGGGAACCTCTGGCACCT 78
QY 21 TrpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProProLysLysSer 40
DB 79 TGGGCTGTGAAGGCTCTGAAGGCTCTTCAAGCTGGAGTCTGTCTCTCTAAGAAATCT 138
QY 41 AlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAspTrpGlnCysProGlyLys 60
DB 139 GCCCAGTGCCTTAGATACAGAAACCTGAGTGCAGAGTGAAGTCTGCCAGGGAAG 198
QY 61 LysArgCysCysProAspThrCysGlyLysLysCysLeuAspProValAspThrProAsn 80
DB 199 AAGAGATGTTGCTGACACTTGTGGCATCAAAATGCTGGATCTCTGTGACACCCCAAC 258
QY 81 ProThrArgArgLysProGlyLysCysProValThrTyrGlnCysLeuMetLeuAsn 100
DB 259 CCAACAAGGAGGAGGCTTGGAGAGTGCCTGAGTCAATGCTTATGCTTGAATGCTTAAAC 318
QY 101 ProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGly 120
DB 319 CCCCCCAATTTCTGTGAGATGGATGGCCAGTGCAGGCTGACTTGAAGTGTTCATGGGC 378
QY 121 MetCysGlyLysSerCysValSerProValLysAla 132
DB 379 ATGTGTGGAAATCTCGCTTCCCTGTGAAAGCT 414

RESULT 7
US-09-954-456-1989
; Sequence 1989, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand
; FILE OF INVENTION: Sets
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1989
; LENGTH: 594
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-1989

Alignment Scores:
Pred. No.: 3,55e-82 Length: 594
Score: 762.00 Matches: 132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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DB: 9 Gaps: 0
US-10-613-105-2 (1-132) x US-09-954-456-1989 (1-594)
QY 1 MetLysSerSerGlyLeuPheProPheLeuValLeuLeuAlaLeuGlyThrLeuAlaPro 20
DB 19 ATGAAGTCCAGCGGCTCTTCCCTTCTGGTGTCTGCTGGGAACCTCTGGCACCT 78
QY 21 TrpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProProLysLysSer 40
DB 79 TGGGCTGTGAAGGCTCTGGAAGTCTCTTCAAGCTGGAGTCTGTCTCTCTAAGAAATCT 138
QY 41 AlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAspTrpGlnCysProGlyLys 60
DB 139 GCCCAGTGCCTTAGATACAGAAACCTGAGTGCAGAGTGAAGTCTGCCAGGGAAG 198
QY 61 LysArgCysCysProAspThrCysGlyLysLysCysLeuAspProValAspThrProAsn 80
DB 199 AAGAGATGTTGCTGACACTTGTGGCATCAAAATGCTGGATCTCTGTGACACCCCAAC 258
QY 81 ProThrArgArgLysProGlyLysCysProValThrTyrGlnCysLeuMetLeuAsn 100
DB 259 CCAACAAGGAGGAGGCTTGGAGAGTGCCTGAGTCAATGCTTATGCTTGAATGCTTAAAC 318
QY 101 ProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGly 120
DB 319 CCCCCCAATTTCTGTGAGATGGATGGCCAGTGCAGGCTGACTTGAAGTGTTCATGGGC 378
QY 121 MetCysGlyLysSerCysValSerProValLysAla 132
DB 379 ATGTGTGGAAATCTCGCTTCCCTGTGAAAGCT 414

RESULT 8
US-09-865-812-1
; Sequence 1, Application US/09865812
; Patent No. US20020115626A1
; GENERAL INFORMATION:
; APPLICANT: Raetelli, Luca
; APPLICANT: Smithson, Glennda
; TITLE OF INVENTION: Method of Detecting Inflammatory Lung Disorders
; FILE REFERENCE: 21402-018 US
; CURRENT APPLICATION NUMBER: US/09/865,812
; CURRENT FILING DATE: 2001-05-28
; PRIOR APPLICATION NUMBER: 60/207,104
; PRIOR FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 594
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-865-812-1

Alignment Scores:
Pred. No.: 3,55e-82 Length: 594
Score: 762.00 Matches: 132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-10-613-105-2 (1-132) x US-09-865-812-1 (1-594)
QY 1 MetLysSerSerGlyLeuPheProPheLeuValLeuLeuAlaLeuGlyThrLeuAlaPro 20
DB 19 ATGAAGTCCAGCGGCTCTTCCCTTCTGGTGTCTGCTGGGAACCTCTGGCACCT 78
QY 21 TrpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProProLysLysSer 40
DB 79 TGGGCTGTGAAGGCTCTGGAAGTCTCTTCAAGCTGGAGTCTGTCTCTCTAAGAAATCT 138
QY 41 AlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAspTrpGlnCysProGlyLys 60
DB 139 GCCCAGTGCCTTAGATACAGAAACCTGAGTGCAGAGTGAAGTCTGCCAGGGAAG 198
QY 61 LysArgCysCysProAspThrCysGlyLysLysCysLeuAspProValAspThrProAsn 80
DB 199 AAGAGATGTTGCTGACACTTGTGGCATCAAAATGCTGGATCTCTGTGACACCCCAAC 258
QY 81 ProThrArgArgLysProGlyLysCysProValThrTyrGlnCysLeuMetLeuAsn 100
DB 259 CCAACAAGGAGGAGGCTTGGAGAGTGCCTGAGTCAATGCTTATGCTTGAATGCTTAAAC 318
QY 101 ProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGly 120
DB 319 CCCCCCAATTTCTGTGAGATGGATGGCCAGTGCAGGCTGACTTGAAGTGTTCATGGGC 378
QY 121 MetCysGlyLysSerCysValSerProValLysAla 132
DB 379 ATGTGTGGAAATCTCGCTTCCCTGTGAAAGCT 414
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Db 139 GCCAGTGCCTTAGATACAAAGAAACCTGAGTGGCAGAGTGACTGGCAGTGTCCAGGGAAG 198
QY 61 LysArgCysCysProAspThrCysGlyLysCysLeuAspProValAspThrProAsn 80
Db 199 AAGAGATGTTGCTGACACTTGTGGCATCAAAATGCCCTGGATCTGTGTGACACCCCAAC 258
QY 81 ProThrArgArgLysProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAsn 100
Db 259 CCAACAAGGAGGAAGCTCGGAAGTGCCTGAGTGCCTATATGCGCAATGTTTGGATGCTTAAC 318
QY 101 ProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGly 120
Db 319 CCCCCCAATTTCTGTGAGATGGATGCCAGTGCAGTGAAGCGTGACTGAAGTGTTCATGGGC 378
QY 121 MetCysGlyLysSerCysValSerProValLysAla 132
Db 379 ATGTGTGGGAATCTCGCTTTCCCTGTGAAAGCT 414

RESULT 9
US-10-097-340-295
; Sequence 295, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
; APPLICANT: John MONAHAN
; APPLICANT: Manjula GANNAVAPURU
; APPLICANT: Sebastian HOERSCH
; APPLICANT: Shubhangi KAMATKAR
; APPLICANT: Steve G. KOVATS
; APPLICANT: Rachel E. MEYERS
; APPLICANT: Michael MORRISEY
; APPLICANT: Peter OLANDT
; APPLICANT: Ami SEN
; APPLICANT: Peter VEIBY
; APPLICANT: Gordon B. MILLS
; APPLICANT: Robert C. BAST, Jr.
; APPLICANT: Karen LU
; APPLICANT: Rosemarie SCHMANDT
; APPLICANT: Xumei ZHAO
; APPLICANT: Karen GLATT
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; FILE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
; FILE REFERENCE: MRI-030
; CURRENT APPLICATION NUMBER: US/10/097,340
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,025
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/325,149
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/276,026
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/324,967
; PRIOR FILING DATE: 2001/09/26
; PRIOR APPLICATION NUMBER: 60/311,732
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325,102
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/323,580
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 295
; LENGTH: 594
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-097-340-295

Alignment Scores:
Pred. No.: 3 55e-82 Length: 594
Score: 762.00 Matches: 132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-613-105-2 (1-132) x US-10-097-340-295 (1-594)
QY 1 MetLysSerSerGlyLeuPheProPheLeuValLeuLeuAlaLeuGlyThrLeuAlaPro 20
Db 19 ATGAAGTCAGGGCCCTCTTCCCTTCCTGGTGTCTTGGCCCTGGAACTCTGGCACCT 78
QY 21 TrpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProLysLysSer 40
Db 79 TGGGCTGTGGAAGGCTCTGGAAGTCTTCAAAGCTGGAGTCTGTCTCTCTAAGAAATCT 138
QY 41 AlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAspTrpGlnCysProGlyLys 60
Db 139 GCCAGTGCCTTAGATACAAAGAAACCTGAGTGCAGAGTGACTGGCAGTGTTCAGGGAAG 198
QY 61 LysArgCysCysProAspThrCysGlyLysCysLeuAspProValAspThrProAsn 80
Db 199 AAGAGATGTTGCTGACACTTGTGGCATCAAAATGCCCTGGATCTGTGTGACACCCCAAC 258
QY 81 ProThrArgArgLysProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAsn 100
Db 259 CCAACAAGGAGGAAGCTCGGAAGTGCCTGAGTGCCTATATGCGCAATGTTTGGATGCTTAAC 318
QY 101 ProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGly 120
Db 319 CCCCCCAATTTCTGTGAGATGGATGCCAGTGCAGTGAAGCGTGACTGAAGTGTTCATGGGC 378
QY 121 MetCysGlyLysSerCysValSerProValLysAla 132
Db 379 ATGTGTGGGAATCTCGCTTTCCCTGTGAAAGCT 414

RESULT 10
US-10-205-823-374
; Sequence 374, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John B.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Womsey, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 374
; LENGTH: 594
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-205-823-374

Alignment Scores:
Pred. No.: 3 55e-82 Length: 594
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Score: 762.00 Matches: 132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-10-613-105-2 (1-132) x US-10-205-823-374 (1-594)

QY 1 MetLysSerSerGlyLeuPheProPheLeuValLeuAlaLeuGlyThrLeuAlaPro 20
Db 19 ATGAAGTCCAGCGGCTCTTCCCTTCTGGTCTGCTTCCCTGGGAACCTTGGCACCT 78
QY 21 TrpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProProLysLysSer 40
Db 79 TGGGCTGTGGAAGGCTCTGGAAGTCTTCAAAAGCTGGAGTCTGCTCTCTCAAGAAATCT 138
QY 41 AlaGlnCysLeuArgTrpLysLysProGluCysGlnSerAspTrpGlnCysProGlyLys 60
Db 139 GCCAGTGCCTTAGATACAAAGAACCTGAGTGCAGAGTGAAGTGTCCAGGGAAG 198
QY 61 LysArgCysCysProAspThrCysGlyLysCysLeuAspProValAspThrProAsn 80
Db 199 AAGAGATGTTGCTGACACTTGTGGCATCAATGCTGGATCTGTGTGACACCCCAAC 258
QY 81 ProThrArgLysProGlyLysCysProValThrTrpGlyGlnCysLeuMetLeuAsn 100
Db 259 CCAACAAGGAGGAAGCTGCGGAAGTGCAGTGCCTTATGGCCAATGTTTGTATGCTTAAC 318
QY 101 ProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGly 120
Db 319 CCCCCCAATTTCTGTGAGATGGATGGCCAGTGCAGGCGTGAAGTGTTCATGGGC 378
QY 121 MetCysGlyLysSerCysValSerProValLysAla 132
Db 379 ATGTGTGGGAATCTCGCTTCCCTGTGGAAGCT 414

RESULT 11

US-10-177-293-429
; Sequence 429, Application US/10177293
; Publication No. US20030124128A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Gannavarpu, Manjula
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Mertens, Maureen
; APPLICANT: Myer, Vic
; APPLICANT: Wang, Youzhen
; APPLICANT: Xu, Yongyao
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Monahan, John
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Bast Jr., Robert C.
; APPLICANT: Hortobagyi, Gabriel N.
; APPLICANT: Pusztai, Lajos
; APPLICANT: Meric, Funda
; APPLICANT: Sahin, Aysegul
; APPLICANT: Mills, Gordon B.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
; FILE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-038
; CURRENT APPLICATION NUMBER: US/10/177,293
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585

; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 429
; LENGTH: 594
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-177-293-429

Alignment Scores: 3.55e-82 Length: 594
Pred. No.: 762.00 Matches: 132
Score: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-10-613-105-2 (1-132) x US-10-177-293-429 (1-594)

QY 1 MetLysSerSerGlyLeuPheProPheLeuValLeuAlaLeuGlyThrLeuAlaPro 20
Db 19 ATGAAGTCCAGCGGCTCTTCCCTTCTGGTCTGCTTCCCTGGGAACCTTGGCACCT 78
QY 21 TrpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProProLysLysSer 40
Db 79 TGGGCTGTGGAAGGCTCTGGAAGTCTTCAAAAGCTGGAGTCTGCTCTCTCAAGAAATCT 138
QY 41 AlaGlnCysLeuArgTrpLysLysProGluCysGlnSerAspTrpGlnCysProGlyLys 60
Db 139 GCCAGTGCCTTAGATACAAAGAACCTGAGTGCAGAGTGAAGTGTCCAGGGAAG 198
QY 61 LysArgCysCysProAspThrCysGlyLysCysLeuAspProValAspThrProAsn 80
Db 199 AAGAGATGTTGCTGACACTTGTGGCATCAATGCTGGATCTGTGTGACACCCCAAC 258
QY 81 ProThrArgLysProGlyLysCysProValThrTrpGlyGlnCysLeuMetLeuAsn 100
Db 259 CCAACAAGGAGGAAGCTGCGGAAGTGCAGTGCCTTATGGCCAATGTTTGTATGCTTAAC 318
QY 101 ProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGly 120
Db 319 CCCCCCAATTTCTGTGAGATGGATGGCCAGTGCAGGCGTGAAGTGTTCATGGGC 378
QY 121 MetCysGlyLysSerCysValSerProValLysAla 132
Db 379 ATGTGTGGGAATCTCGCTTCCCTGTGGAAGCT 414

RESULT 12

US-10-172-118-863
; Sequence 863, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 863
; LENGTH: 594
; TYPE: DNA
; ORGANISM: Homo sapiens


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; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 863
; LENGTH: 594
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-863

Alignment Scores:
Pred. No.: 3,55e-82 Length: 594
Score: 762.00 Matches: 132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-10-613-105-2 (1-132) x US-10-342-887-863 (1-594)

QY 1 MetLysSerSerGlyLeuPheProPheLeuValLeuAlaLeuGlyThrLeuAlaPro 20
DB 19 ATGAAGTCCAGCGGCTCTTCCCTTCTGGTGTGCTTGGCCCTGGGAACCTCTGGCACCT 78
QY 21 TrpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProLysLysSer 40
DB 79 TGGGCTGTGGAAGGCTCTGGAAGTCTTCAAAGCTGGAGTCTGTCTCTTAAGAAATCT 138
QY 41 AlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAspTyrGlnCysProGlyLys 60
DB 139 GCCCAGTGCCTTAGATACAAAGAACCTGAGTGCCAGAGTACTGGCAGTGTCCAGGGAAG 198
QY 61 LysArgCysCysProAspThrCysGlyLysLysCysLeuAspProValAspThrProAsn 80
DB 199 AAGAGATGTTGTCCTGACACTTGTGCATCAATGCTGATCCTGTTGACACCCCAAC 258
QY 81 ProThrArgArgLysProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAsn 100
DB 259 CCAACAAGAGGAGGAGCTGGGAAGTCCCAAGTGGAGTCTTATGGCAATGTTGATGCTTAAC 318
QY 101 ProProAsnPheCysGluMetAspGlyGlnCysLysAspLeuLysCysCysMetGly 120
DB 319 CCCCCCAATTTCTGTGAGATGGATGGCCAGTGGCAGTGTGAAGTGTTCATGGGC 378
QY 121 MetCysGlyLysSerCysValSerProValLysAla 132
DB 379 ATGTGTGGGAATCTCGCTTTCCCTGTGAAAGCT 414

RESULT 18
US-10-322-696-125
; Sequence 125, Application US/10322696
; Publication No. US20040166490A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Malandro, Marc
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 529452001200
; CURRENT APPLICATION NUMBER: US/10/322,696
; CURRENT FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 125
; LENGTH: 594
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-322-696-125

Alignment Scores:
Pred. No.: 3,55e-82 Length: 594
Score: 762.00 Matches: 132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-10-613-105-2 (1-132) x US-10-322-696-125 (1-594)

QY 1 MetLysSerSerGlyLeuPheProPheLeuValLeuAlaLeuGlyThrLeuAlaPro 20
DB 19 ATGAAGTCCAGCGGCTCTTCCCTTCTGGTGTGCTTGGCCCTGGGAACCTCTGGCACCT 78
QY 21 TrpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProLysLysSer 40
DB 79 TGGGCTGTGGAAGGCTCTGGAAGTCTTCAAAGCTGGAGTCTGTCTCTTAAGAAATCT 138
QY 41 AlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAspTyrGlnCysProGlyLys 60
DB 139 GCCCAGTGCCTTAGATACAAAGAACCTGAGTGCCAGAGTACTGGCAGTGTCCAGGGAAG 198
QY 61 LysArgCysCysProAspThrCysGlyLysLysCysLeuAspProValAspThrProAsn 80
DB 199 AAGAGATGTTGTCCTGACACTTGTGCATCAATGCTGATCCTGTTGACACCCCAAC 258
QY 81 ProThrArgArgLysProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAsn 100
DB 259 CCAACAAGAGGAGGAGCTGGGAAGTCCCAAGTGGAGTCTTATGGCAATGTTGATGCTTAAC 318
QY 101 ProProAsnPheCysGluMetAspGlyGlnCysLysAspLeuLysCysCysMetGly 120
DB 319 CCCCCCAATTTCTGTGAGATGGATGGCCAGTGGCAGTGTGAAGTGTTCATGGGC 378
QY 121 MetCysGlyLysSerCysValSerProValLysAla 132
DB 379 ATGTGTGGGAATCTCGCTTTCCCTGTGAAAGCT 414

RESULT 17
US-10-613-105-1
; Sequence 1, Application US/10613105
; Publication No. US2004015690A1
; GENERAL INFORMATION:
; APPLICANT: Rastelli, Luca
; APPLICANT: Smithson, Glennda
; TITLE OF INVENTION: Method of Detecting Inflammatory Lung Disorders
; FILE REFERENCE: 21402-018 DIV
; CURRENT APPLICATION NUMBER: US/10/613,105
; CURRENT FILING DATE: 2003-07-02
; PRIOR APPLICATION NUMBER: 60/207,104
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 09/865,812
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 594
```



```
Db 1119 TTCTTTTCTGATGATCGAGACAGAACTAAAGACCCATGTTTATGGGTAAAGTTGTC 1178
Qy 20 ProTriAlaValGluGlySerGlyLysSerPhelysAlaGlyValCysProProLysLys 39
Db 1179 AACCCAACTCAGAGATGTCGGGAAGCTCTTCAAGGCCGGTGTGTTGTCACCAAGAG 1238
Qy 40 SerAlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAspTrrpGlnCysProGly 59
Db 1239 TCCGCTCAATGTTTGTAGATCAAGAAGCCAGATGTCAATCCGACTGGCAATGTCCAGGT 1298
Qy 60 LysLysArgCysCysProAspThrCysGlyLleLysCysLeuAspProValAspThrPro 79
Db 1299 AAGAAGAGATGTTGTCAGACACTTGTGGTATCAAGTGTCTAGACCCAGTTGACACCCA 1358
Qy 80 AsnProThrArgArgLysProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeu 99
Db 1359 AACCCAACTAGAGAAAGCCAGGTAGTGTCCAGTTACTTACGGTCAATGTTGATGTTG 1418
Qy 100 AsnProProAsnPhcCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCysMet 119
Db 1419 AACCCACCAAACTCTGTGAATGGACGGTCAATGTAAAGAGAGACTTGAAGTGTGTATG 1478
Qy 120 GlyMetCysGlyLysSerCysValSerProValLysAla 132
Db 1479 GGTATGTGTGGTAACTCTGTGTTTCCCAAGTCAAGGCC 1517

RESULT 23
US-10-025-514-3
; Sequence 3, Application US/10025514
; Publication No. US20030073217A1
; GENERAL INFORMATION:
; APPLICANT: Philip J. BARR
; APPLICANT: Helen GIBSON
; APPLICANT: Phillip PEMBERTON
; TITLE OF INVENTION: MULTIFUNCTIONAL PROTEASE INHIBITORS AND
; TITLE OF INVENTION: THEIR USE IN TREATMENT OF DISEASE
; FILE REFERENCE: 36829200200
; CURRENT APPLICATION NUMBER: US/10/025,514
; PRIOR FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: U.S. 60/256,699
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: U.S. 60/331,966
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-025-514-3

Alignment Scores:
Pred. No.: 3,14e-67 Length: 321
Score: 635.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 83.33% Indels: 0
DB: 14 Gaps: 0

US-10-613-105-2 (1-132) x US-10-025-514-3 (1-321)

Qy 26 SerGlyLysSerPhelysAlaGlyValCysProProLysLysSerAlaGlnCysLeuArg 45
Db 1 TCTGGAAGTCTTTCAGGCCGGTGTGTTGTCACCAAGAGTCCGCTCAATGTTTGAGA 60
Qy 46 TyrLysLysProGluCysGlnSerAspTrrpGlnCysProGlyLysArgCysCysPro 65
Db 61 TACAAGAAGCCAGAAATGTCAATCCGACTGGCAATGTCCAGTAAAGAGATGTTGTCCA 120
Qy 66 AspThrCysGlyLleLysCysLeuAspProValAspThrProAsnProThrArgArgLys 85
Db 121 GACACTTGTGTATCAAGTGTCTAGACCCCAAGTGTGACACCCCAAAACCACTAGAGAAAG 180
```

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Qy 86 ProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAsnProProAsnPhcCys 105
Db 181 CCAGGTAAGTGTCCAGTTACTTACGGTCAATGTTGATGTTGAACCCACCAAACTTCTGT 240
Qy 106 GluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGlyMetCysGlyLysSer 125
Db 241 GAAATGGACCGTCAATGTAAAGAGAGACTTGAAGTGTGTTGATGGGTATGTGTGGTAAGTCC 300
Qy 126 CysValSerProValLysAla 132
Db 301 TGTGTTTCCCAAGTCAAGGCC 321

RESULT 24
US-10-309-290-145
; Sequence 145, Application US/10309290
; Publication No. US20040023241A1
; GENERAL INFORMATION:
; APPLICANT: Alsbobrook II, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Chillakuru, Rajeev A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Gorman, Linda
; APPLICANT: Gould-Rothberg, Bonnie E.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Jeffers, Michael E.
; APPLICANT: Ji, Weizhen
; APPLICANT: Li, Li
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Miller, Charles E.
; APPLICANT: Murphey, Ryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Smithson, Glenda
; APPLICANT: Starling, Gary
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zhong, Haihong
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
; FILE REFERENCE: 21402-502A
; CURRENT APPLICATION NUMBER: US/10/309,290
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/336,600
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/338,285
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/341,346
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/341,477
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/341,540
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/342,592
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/344,297
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/344,903
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/373,288
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/380,981
; PRIOR FILING DATE: 2002-05-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: Curaseqlist version 0.1
; SEQ ID NO 145
```

```
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(321)
US-10-309-290-145

Alignment Scores:
Pred. No.: 3,14e-67 Length: 321
Score: 635.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 83.33% Indels: 0
Gaps: 16
DB: 0

US-10-613-105-2 (1-132) x US-10-309-290-145 (1-321)
QY 26 SerGlyLysSerPheLysAlaGlyValCysProProLysLysSerAlaGlnCysLeuArg 45
DB 1 TCTGGAAGTCCCTTCAAGAGTGGAGTCTGCTCCTTAAGAAATCTGCCAGTGCCTTAGA 60
QY 46 TyrLysLysProGluCysGlnSerAspTyrGlnCysProGlyLysLysArgCysCysPro 65
DB 61 TACAAGAAACCTGAGTCCAGAGTACTGGCAGTGTCCAGGGAAGAGAGATGTTGCTCT 120
QY 66 AspThrCysGlyLysLysCysLeuAspProValAspThrProAsnProThrArgArgLys 85
DB 121 GACACTTGTGGCATCAATGCTGGATCCTGTTGACACCCCAACCCCAAGGGAAG 180
QY 86 ProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAsnProProAsnPheCys 105
DB 181 CTGGGAAGTCCAGTACTTATGGCAATGTTGATGTTAAACCCCAATTTCTGT 240
QY 106 GluMetAspGlyGlnCysLysArgAspLeuLysCysMetGlyMetCysGlyLysSer 125
DB 241 GAGATGGATGCCAGTGCAGCGTGAAGTGAAGTGTTCATGGCATGGCATGGTGGGAAATCC 300
QY 126 CysValSerProValLysAla 132
DB 301 TGGCTTTCCCTGTGAAGACT 321

RESULT 25
US-10-025-514-7
; Sequence 7, Application US/10025514
; Publication No. US20030073217A1
; GENERAL INFORMATION:
; APPLICANT: Philip J. BARR
; APPLICANT: Helen GIBSON
; APPLICANT: Philip PEMBERTON
; TITLE OF INVENTION: MULTIFUNCTIONAL PROTEASE INHIBITORS AND
; TITLE OF INVENTION: THEIR USE IN TREATMENT OF DISEASE
; FILE REFERENCE: 36829200200
; CURRENT APPLICATION NUMBER: US/10/025,514
; PRIOR FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: U.S. 60/256,699
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: U.S. 60/331,966
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1525
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-025-514-7

Alignment Scores:
Pred. No.: 2,02e-66 Length: 1525
Score: 635.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 83.33% Indels: 0
DB: 0

; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(321)
US-10-309-290-145

Alignment Scores:
Pred. No.: 3,14e-67 Length: 321
Score: 635.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 83.33% Indels: 0
DB: 0

US-10-613-105-2 (1-132) x US-10-025-514-7 (1-1525)
QY 26 SerGlyLysSerPheLysAlaGlyValCysProProLysLysSerAlaGlnCysLeuArg 45
DB 12 TCTGGAAGTCTTTCAAGGCCGGTGTTCCTCACCAAGAAAGTCCGCTCAATGTTTGA 71
QY 46 TyrLysLysProGluCysGlnSerAspTyrGlnCysProGlyLysLysArgCysCysPro 65
DB 72 TACAAGAACCCAGAAATGTCAATCCGACTGGCAATGTCCAGGTAAAGAGAGATGTTGTCCA 131
QY 66 AspThrCysGlyLysLysCysLeuAspProValAspThrProAsnProThrArgArgLys 85
DB 132 GACACTTGTGGTATCAAGTGTCTAGACCCAGTTCACACCCCAACCCCAAGAAAG 191
QY 86 ProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAsnProProAsnPheCys 105
DB 192 CCAGGTAAAGTGTCCAGTTACTTACGGTCAATGTTTGTGATGTTGAACCCCAACCTTCTGT 251
QY 106 GluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGlyMetCysGlyLysSer 125
DB 252 GAAATGGACGGTCAATGTAAAGAGAGACTTGAAGTGTGTTATGGGTATGTTGTAAGTCC 311
QY 126 CysValSerProValLysAla 132
DB 312 TGTGTTTCCCTCAAGGCC 332

RESULT 26
US-10-322-696-124
; Sequence 124, Application US/10322696
; Publication No. US20040166490A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Malandro, Marc
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 529452001200
; CURRENT APPLICATION NUMBER: US/10/322,696
; CURRENT FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124
; LENGTH: 22324
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-322-696-124

Alignment Scores:
Pred. No.: 2,6e-53 Length: 22324
Score: 537.50 Matches: 103
Percent Similarity: 42.51% Conservative: 2
Best Local Similarity: 41.70% Mismatches: 1
Query Match: 70.54% Indels: 141
DB: 17 Gaps: 1

US-10-613-105-2 (1-132) x US-10-322-696-124 (1-22324)
QY 26 SerGlyLysSerPheLysAlaGlyValCysProProLysLysSerAlaGlnCysLeuArg 45
DB 10819 TCTTCAAAAGCCTTCAAGCTGGAGTCTGCTCTCTTAAGAAATCTGCCAGTGCCTTAGA 10878
QY 46 TyrLysLysProGluCysGlnSerAspTyrGlnCysProGlyLysLysArgCysCysPro 65
DB 10879 TACAAGAACCTGAGTGCACAGAGTACTGGCAGTGTCCAGGGAAGAGAGATGTTGCTCT 10938
QY 66 AspThrCysGlyLysLysCysLeuAspProValAspThrProAsnProThr 82
DB 10939 GACACTTGTGGCATCAATGCTGGATCCTGTTGACACCCCAACCCCAAGTAAGCAGGTC 10998
QY 82 ----- 82
DB 10999 GGGGAACCTGGGTAGAGGAGTGGCTGGGGACACAGCATTTAGAGGGATGGAACTGGGT 11058
```

QY 82 ----- 82
Db 11059 GATGGGTCTGCCAGGCTCTTGTCAATCCGTCAAGTACACTGCCCTAAGCAGGA 11118
QY 82 ----- 82
Db 11119 AGTAGCCAGCAGCTGGTGAAGCAGCGGGCATTTAGATACCCAGGTAGTTGGAGCCCTCC 11178
QY 82 ----- 82
Db 11179 CACCTAGTCAGCACTGGGTGGTGGCCACCTGCATCAATGGGGGCTGAAGTTCTAGGA 11238
QY 82 ----- 82
Db 11239 GAGCCAGGTCTATGTTTGGGGGCGCGCTTAGGGAGAGGTGGTGTATAGAGGTGGG 11298
QY 82 ----- 82
Db 11299 AGGGGATGATCCCCCTGCTGAAGTGGAGCAGGGGCTCACTTAAAGTGGGGATGGG 11358
QY 83 -----ArgArg 84
Db 11359 AGGGTTGTATAAGTACAGGCTCTGACCGGTAGCCTCACTCTCACCAGCAGGAGG 11418
QY 85 LysProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAenProProAenPhe 104
Db 11419 AAGCTGGGAAGTGCCCGAGTGACTTATGGCCAATGTTGATGCTTAACCCCGCAATTC 11478
QY 105 CysGluMetAspGlyGlnCysLysAspLeuLysCysMetGlyMetCysGlyLys 124
Db 11479 TGTGAGATGATGCCAGTCAGCGAGTGAAGTGTTCATGGCGCATGTGGGAAA 11538
QY 125 SerCysValSerProValLys 131
Db 11539 TCCTGGCTTCCCTGTGAAA 11559

RESULT 27

US-10-322-696-122
; Sequence 122, Application US/10322696
; Publication No. US20040166490A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Malandro, Marc
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 529452001200
; CURRENT APPLICATION NUMBER: US/10/322,696
; CURRENT FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 122
; LENGTH: 1079
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-322-696-122

Alignment Scores:
Pred. No.: 5,49e-46 Length: 1079
Score: 463.50 Matches: 79
Percent Similarity: 72.73% Conservative: 17
Best Local Similarity: 59.85% Mismatches: 33
Query Match: 60.83% Indels: 3
DB: 17 Gaps: 2

US-10-613-105-2 (1-132) x US-10-322-696-122 (1-1079)

QY 1 MetLysSerSerGlyLeuPheProPheLeuValLeuLeuAlaLeuGlyThrLeuAlaPro 20
Db 440 ATGAAGTCCTCGCGCCCTTTTACCTTTTACGCTGCTCTTGTGCTGGGATCCTGGCACCC 499
QY 21 TrpAlaValGluGlySerGlyLys-----SerPheLysAlaGlyValCysProProLys 38
Db 500 TGGAGTGTGAAGGA---GGCAAAATATGATGCTATCAAAATCGGAGCCCTGCCCTGTCTAAA 556

QY 39 LysSerAlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAspTrpGlnCysPro 58
Db 557 AAGCTGCCCGAGTGCCTTAAGCTTGAGAAAGCCCAACTGCCGTACTGACTGGAGTGGCCG 616
QY 59 GlyLysLysArgCysCysProAspThrCysGlyLysCysLeuAspProValAspThr 78
Db 617 GGAACACAGAGGTGCTGCCAAGATGTTGCGGTTCCAAGTGCCTGAATCCTGTTCCCAT 676
QY 79 ProAsnProThrArgArgLysProGlyLysCysProValThrTyrGlyGlnCysLeuMet 98
Db 677 CGCAAAACCAAGTGTGGAGGAGCCTGGAGTGCCTCAAAACTCAGGCAAGATGTATGATG 736
QY 99 LeuAenProProAenPheCysGluMetAspGlyGlnCysLysAspLeuLysCysCys 118
Db 737 CTTAAACCTCCCAATCTCTGCCAGAGGAGCGGCAGTGTGACGGCAAAATACAAGTGTCT 796
QY 119 MetGlyMetCysGlyLysSerCysValSerProVal 130
Db 797 GAGGTATATGTGGGAAGTCTGCTGCTGCCCGCATG 832

RESULT 28

US-10-305-720-1024
; Sequence 1024, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 1024
; LENGTH: 325
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040010136A1 939088
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1) ... (325)
; OTHER INFORMATION: a, t, c, g, or other
US-10-305-720-1024

Alignment Scores:
Pred. No.: 6.01e-46 Length: 325
Score: 458.00 Matches: 96
Percent Similarity: 89.81% Conservative: 1
Best Local Similarity: 88.89% Mismatches: 10
Query Match: 60.10% Indels: 4
DB: 16 Gaps: 0

US-10-613-105-2 (1-132) x US-10-305-720-1024 (1-325)

QY 1 MetLysSerSerGlyLeuPheProPheLeuValLeuLeuAlaLeuGlyThrLeuAlaPro 20
Db 1 ATGAAGTCCAGCGGNCCTTNCCTTNCCTTNCCTTNCCTTNCCTTNCCTTNCCTTNCCT 60
QY 21 TrpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCys-ProProLysLysSe 40
Db 61 TGGGCTGTGGAGGCTCTGGAAAGTCTTCAAAGCTGGAGTCTGCTCCCTCAAAGGAATC 120
QY 40 rAlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAspTrpGlnCysProGlyL 60
Db 121 TGCCCAAGTGTCTAGATACAAAGAAACCTGAGTCCCAAGTGCAGTGGCAGTGTCCAGGAA 180
QY 60 sLysArgCysCysProAspThrCysGlyLysCysLeuAspProValAspThrProAs 80
Db 181 GAAGAGATGTTGTCTTGACACTTGTGGCATCAAAATGCTGTGATCTTNTTGACAC-CCAAA 239

Qy 80 nProThrArgArgLysProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAs 100
|||||
Db 240 CCACACAGAGAGAGCT-GGGAGTGCAGTACCTATTAGNCATGTTTGTATTAAN 298
Qy 100 nProProAsnPhCysGluMet 107
|||||
Db 299 CCCCCCAA--TTTTGTGAGATG 318

RESULT 29

US-10-125-159-37
; Sequence 37, Application US/10125159
; Publication No. US20030166023A1
; GENERAL INFORMATION:
; APPLICANT: Iartchouk, Natalia
; APPLICANT: Ayers, Mark D.
; APPLICANT: Brown, Jeffrey L.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR THE
; IDENTIFICATION, ASSESSMENT, PREVENTION AND THERAPY OF
; TITLE OF INVENTION: HUMAN CANCERS
; FILE REFERENCE: MRI-029
; CURRENT APPLICATION NUMBER: US/10/125,159
; CURRENT FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: 60/295,031
; PRIOR FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: 60/284,773
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/284,764
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-125-159-37

Alignment Scores:
Pred. No.: 3,94e-33 Length: 422
Score: 352.50 Matches: 82
Percent Similarity: 67.44% Conservative: 5
Best Local Similarity: 63.57% Mismatches: 40
Query Match: 46.26% Indels: 5
DB: 15 Gaps: 0

US-10-613-105-2 (1-132) x US-10-125-159-37 (1-422)

Qy 6 LeuPheProPheLeuValLeuLeuAlaLeuGlyThrLeuAlaProTrpAlaValGluGly 25
Db 27 CTTTTTCTCTTCTGTGCTGAAAGAAAGGAACTCTGGCACCTTGGGCTGAGGAAGGC 86
Qy 26 SerGlyLysSerPheLysAlaGlyValCysProProLysLysSerAlaGlnCysLeu-Ar 45
Db 87 TCTGGAAGAAGAACTTCAAGGTGGAGCCGCCCTCTTAACAAAGGGGCCAGTGCCTGGAG 146
Qy 45 gTyrLys-LysProGluCysGlnSerAspTrpGlnCysProGlyLysLysArgCysCysP 65
Db 147 ATACACCAACCACTGGGGGCGAGGAGCTGGCCCC-CCAGGAAGAAGAGAGCCCC-C 204
Qy 65 roAspThrCysGlyIleLysCysLeuAspProValAspThrProAsnProThrArgArgL 85
Db 205 CTGACACTGGGGGAATCAATGCTGGAGGTGAAGACACCTT-AAACCCACCAGGAGGA 263
Qy 85 yAsProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAsnProAsnPhC 105
Db 264 AGCTGGGAAGTGCACAGTACCTATTATGCCAATGTTTGAAGAAAAAGGGGGGGTTAT 323
Qy 105 yGluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGlyMetCysGlyLys 125
Db 324 GAGAAAGAGTGGCCAGCAGCAAGGCTGACTTGAAGCGGTGCTCTCTCATGTGTGGAGAG 383
Qy 125 erCysValSerProValLysAla 132
Db 384 GCTGCGAAACCCCTGCCAAAGCT 406

RESULT 30

US-10-116-802-431
; Sequence 431, Application US/10116802
; Publication No. US20030065157A1
; GENERAL INFORMATION:
; APPLICANT: Amy Lasek
; TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER
; FILE REFERENCE: PA-0045 US
; CURRENT APPLICATION NUMBER: US/10/116,802
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/281,593
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 519
; SOFTWARE: PERL Program
; SEQ ID NO 431
; LENGTH: 805
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 1159769.1
US-10-116-802-431

Alignment Scores:
Pred. No.: 3,57e-31 Length: 805
Score: 339.00 Matches: 104
Percent Similarity: 72.19% Conservative: 5
Best Local Similarity: 68.87% Mismatches: 21
Query Match: 44.49% Indels: 21
DB: 14 Gaps: 3

US-10-613-105-2 (1-132) x US-10-116-802-431 (1-805)

Qy 1 MetLysSerSerGlyLeu-PheProPheLeuValLeuLeuAla-LeuGlyThrLeu-Ala 19
Db 124 ATGAAGTCCAGCGGCTCTTTCCCTTCTCTGTGTGTCTTGGCTTGGGAACCTCTGGACA 183
Qy 20 ProTrpAla-ValGluGly-SerGlyLysSerPheLys-AlaGlyValCys-ProProL 38
Db 184 CCTTGGGCTTGTGGAAGGACTCTGGAAGAGTCCCTTCAATAGCTGGAGTCTGTCCCTCCAA 243
Qy 38 yLysSerAlaGlnCysLeu--ArgTyrLysLysProGlu-CysGlnSerAspTrp-Gl 56
Db 244 GGAATCTGCCAGATGCCTTAGCATACAAGAAACCTGTATGTGCAGAGTACTGGCA 303
Qy 56 nCysProGlyLysLysArgCysCys-ProAspThrCysGlyIle-LysCysLeu-AspPr 75
Db 304 GTGTCCAGGAAGACAGAGATGTTGTCCCTGACACTTGTGGCATCCAAATGCCCTGGATCC 363
Qy 75 oValAspThr-ProAsnProThrArgLysPro-GlyLysCysProVal-ThrTyrGl 94
Db 364 TGTGTACACCCCAACCAACCAAGAGGAGGAGCTGGGAGTCCAGTGTGACTTATGG 423
Qy 94 yGlnCysLeu-MetLeuAsnProProAsnPhCys-----GluMetAspGlyGlnCysL 112
Db 424 CCAATGTTGAAGCTTAACCCCCCAATTTTTGTGAGATGATGTGTCAGATTGCCAA 483
Qy 112 yAsArgAspLeuLysCysCysMetGlyMet---CysGlyLysSerCysValSerProVal 130
Db 484 GCTGTGACTTGAAGTGTTCATGGGCGCATGATGTGTGGAAATCTCTGTGCAATTTCCCTGTG 542

RESULT 31

US-10-076-816-57
; Sequence 57, Application US/10076816
; Publication No. US20030056244A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Ning
; APPLICANT: Rodriguez, Raymond
; APPLICANT: Hagie, Frank E.
; TITLE OF INVENTION: Feed Additive Compositions and Methods
; FILE REFERENCE: 50665-8021.US00
; CURRENT APPLICATION NUMBER: US/10/076,816


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; CURRENT FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/269,188
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/847,232
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/266,929
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/201,182
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 4090
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(4090)
; OTHER INFORMATION: n = A,T,C or G
US-10-076-816-57

Alignment Scores:
Pred. No.: 7,69e-24 Length: 4090
Score: 285.00 Matches: 57
Percent Similarity: 28.24% Conservative: 17
Best Local Similarity: 21.76% Mismatches: 28
Query Match: 37.40% Indels: 160
DB: 14 Gaps: 1

US-10-613-105-2 (1-132) x US-10-076-816-57 (1-4090)
Qy 29 SerPheLysAlaGlyValCysProProlYsSerAlaGlnCysLeuArgTyrLysLys 48
Db 1922 GCTATCAAAATCGAGCCCTGCTGCTAAAGCCCTGCCAGTGCCTTAAGCTTGAGAAG 1981
Qy 49 ProGlnCysGlnSerAspTrpGlnCysProGlnLysLysArgCysCysProAspThrCys 68
Db 1982 CCACAATGCCGTACTGACTGGAGTGCCTGGGAAAGCAGAGGTGCTGCCAAGATGCTTGC 2041
Qy 69 GlyLysLysCysLeuAspProValAspThrProAsnProThrArg----- 83
Db 2042 GGTTCCAAGTGCCTGAATCCTGTTCCTATCCCAACACAGTGGAGCCAGCAGAGAAACAG 2101
Qy 83 ----- 83
Db 2102 AGAGGGGACATCAACGTCAGAGCCACCAGAGTGAATGAAGAGTCCCTCCAGGCATC 2161
Qy 83 ----- 83
Db 2162 CTTGTTTCTAAGAGCTGTTGGGTCCAACATGTCAGTTAGTCAAGGCCCTCTTGCTGCCATT 2221
Qy 83 ----- 83
Db 2222 GGCAGGAAGAGCCATTGCTCGAGTTCGCACTCTGTGAGGATGATGCTTTACAACCAT 2281
Qy 83 ----- 83
Db 2282 TCGGCCCTTTCCGGGCTGGAGAGCTGGTCCCTGCACTTGGCTGGAGGCTAGATGGTAGCG 2341
Qy 83 ----- 83
Db 2342 AGGAAGCGTCTCTTTTCAGGAGGCGTGTGTTGGAGGAGGTGACAAAGGTGATGGGTGG 2401
Qy 83 ----- 83
Db 2402 ATGGGACGCAACTTCCTCGCTCAGGAAGGAGATGTTGGGTTAAAGACATGAGAGATGTGT 2461
Qy 83 ----- 83
Db 2462 GCCTGAGCCCTAAGACATCGGCCCTGTGAATCCTTTCTCAACAGGAGATGTGTTGCTG 2521
Qy 84 -----ArgLysProGlnLys 88
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Db 187 GCCAGTGCCTTAGANACAGAAACCTGAGTGCANAGTACTGGCAGGGGCCAAGGAA 246
Qy 60 LysLysArgCysCysProAspThrCysGlyIleLys 71
Db 247 AAAAAAAAAAGTTGCCCTNANCNTNGGGGAAAAA 282

RESULT 33
US-09-814-353-9156
; Sequence 9156, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9156
; LENGTH: 313
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 14, 20, 24, 50, 51, 53, 58, 61, 73, 95, 117, 134, 202, 222,
; LOCATION: 265, 267, 270, 272, 287, 292, 301, 308
; OTHER INFORMATION: n = A, T, C or G
US-09-814-353-9156

Alignment Scores:
Pred. No.: 5.43e-25 Length: 313
Score: 283.50 Matches: 55
Percent Similarity: 79.17% Conservative: 2
Best Local Similarity: 76.39% Mismatches: 14
Query Match: 37.20% Indels: 1
DB: 10 Gaps: 1

US-10-613-105-2 (1-132) x US-09-814-353-9156 (1-313)
Qy 1 MetLysSerSerGlyLeuPheProPheLeuValLeuAlaLeuGlyThrLeuAlaPro 20
Db 67 TTGAACNCCAGGCGCTCTCCCTTCNGGGGCTGTTGCCCTGGGAACNCTGGCACCT 126
Qy 21 TrpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProProLysLysSer 40
Db 127 TGGGCTGNGAAGGCTCTGAAAGTCTTCAAAGCTGGAGTCTGCTCCTCTAAGAAATCT 186
Qy 41 AlaGlnCysLeuArgGlyLysLysProGluCysGlnSerAspTrpGlnCysPro---Gly 59
Db 187 GCCAGTGCCTTAGANACAGAAACCTGAGTGCANAGTGAAGTGAAGTGGCAGGGGCCAAGGAA 246
Qy 60 LysLysArgCysCysProAspThrCysGlyIleLys 71
Db 247 AAAAAAAAAAGTTGCCCTNANCNTNGGGGAAAAA 282

RESULT 34
US-10-322-696-121
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; Sequence 121, Application US/10322696
; Publication No. US20040166490A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Malandro, Marc
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 529452001200
; CURRENT APPLICATION NUMBER: US/10/322,696
; CURRENT FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 121
; LENGTH: 38692
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-322-696-121

Alignment Scores:
Pred. No.: 8.95e-22 Length: 38692
Score: 277.50 Matches: 57
Percent Similarity: 30.33% Conservative: 17
Best Local Similarity: 23.36% Mismatches: 28
Query Match: 36.42% Indels: 143
DB: 17 Gaps: 1

US-10-613-105-2 (1-132) x US-10-322-696-121 (1-38692)
Qy 29 SerPheLysAlaGlyValCysProProLysLysSerAlaGlnCysLeuArgTyLysLys 48
Db 27153 GCTATCAAAATCGGAGCCTGCTCTAAAAGCCTGCCAGTGCCTTAAGCTTGAGAAG 27212
Qy 49 ProGluCysGlnSerAspTrpGlnCysProGlyLysLysArgCysCysProAspThrCys 68
Db 27213 CCACAATGCGTACTGACTGGGAGTCCCGGGAAACAGAGGTGCTGCCAAGATGCTTGC 27272
Qy 69 GlyIleLysCysLeuAspProValAspThrProAsnPro----- 81
Db 27273 GGTTCCAAGTGCCTGAATCCTGTTCCCATTCGCAAAACAGGTGAGCCAGCAGAGAAACA 27332
Qy 81 ----- 81
Db 27333 GAGAGGGACAATCAACGTCAGAGCCAGAGAGTGAATGAAGAGTCCCTCCAGGCAT 27392
Qy 81 ----- 81
Db 27393 CCTTGTTTCTAAGAGCTGTTGGTCCACATGTCAGTTAGTCAAGGCCTCTTCTGCCAT 27452
Qy 81 ----- 81
Db 27453 TGGCAGGAAGAGCATTTCCTGCTCAGTTGCCACTCTGTGAGGATGATGGCTTTACAACCA 27512
Qy 81 ----- 81
Db 27513 TTCGGGCCCTTTCGGGGCTGGAGAGCTGGTCCCTGTCATTTGGCTGGAGGCTAGATGGTAGC 27572
Qy 81 ----- 81
Db 27573 GAGAAACAGGTCTCTTTTCAGAGGGCGTGTTCAGAGGAGGTGACAAAGGTGATGGTG 27632
Qy 81 ----- 81
Db 27633 GATGGGACGAACCTTCTGCTCAGGAAGAGAGATGTTGGGTTAAAGACATGGAGATGTGT 27692
Qy 82 ----- ThrArgAspLysPro 86
Db 27693 TGCCTGAGCCCTAAGACATCGGCCCTGTGAATCCTTTCTCAACAGTGTGG-AGAAAGCCT 27751
Qy 87 GlyLysCysProValThrTyGlyGlnCysLeuMetLysLeuAsnProProAsnPheCysGlu 106
Db 27752 GGGAGGTGCGTCAAAACTCAGGCAAGATGTATGATGCTTAAACCTCCCAATGTCTGCCAG 27811
Qy 107 MetAspGlyGlnCysLysArgAspLeuLysCysCysMetCysGlyLysSerCys 126
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[illegible]

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; NUMBER OF SEQ ID NOS: 325
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 411
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(411)
; OTHER INFORMATION: n=a,t,g or c
US-09-967-768A-3

Alignment Scores:
Pred. No.: 1,66e-22 Length: 411
Score: 264.00 Matches: 53
Percent Similarity: 74.67% Conservative: 3
Best Local Similarity: 70.67% Mismatches: 17
Query Match: 34.65% Indels: 3
DB: 9 Gaps: 1

US-10-613-105-2 (1-132) x US-09-967-768A-3 (1-411)
Qy 60 LysLysArgCysCysProAspThrCysGlyIleLysCysLeuAspProValAspThrPro 79
Db 406 AAAAGAAATNTTGGCCNGAAACTTGGNGCATNAANTGCCG-GGNCCTCTGTNNACCCC 348
Qy 80 ---AsnProThrArgArgLysPro-GlyLysCysProValThrTyrglyGlnCysLeuMe 98
Db 347 CNAANCCCAACAAGNGNAACCTTGGNAAGTNCNAGTANTTNGCCCAATGTTNGAT 288
Qy 98 tLeuAsnProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCy 118
Db 287 GCTNAACCCCCCAATTTCTGTGAGATGGATGGCCAGTGCACGCGTGAAGTGTG 228
Qy 118 sMetGlyMetCysGlyLysSerCysValSerProValLysAla 132
Db 227 CATGGGCATGTGTGGGAAATCTCGCTTCCCTGTGAAAGCT 185

RESULT 38
US-09-960-706-16/c
; Sequence 16, Application US/09960706
; Publication No. US20030134280A1
; GENERAL INFORMATION:
; APPLICANT: Munger, William E.
; TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplasia
; FILE REFERENCE: 44921-5029-01US
; CURRENT APPLICATION NUMBER: US/09/960,706
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 60/223,323
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 09/873,319
; PRIOR FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 411
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(411)
; OTHER INFORMATION: n = a or c or g or t
US-09-960-706-16

Alignment Scores:
Pred. No.: 1,66e-22 Length: 411
Score: 264.00 Matches: 53
Percent Similarity: 74.67% Conservative: 3
Best Local Similarity: 70.67% Mismatches: 17
Query Match: 34.65% Indels: 3
DB: 10 Gaps: 1

US-10-613-105-2 (1-132) x US-09-967-768A-3 (1-411)
Qy 60 LysLysArgCysCysProAspThrCysGlyIleLysCysLeuAspProValAspThrPro 79
Db 406 AAAAGAAATNTTGGCCNGAAACTTGGNGCATNAANTGCCG-GGNCCTCTGTNNACCCC 348
Qy 80 ---AsnProThrArgArgLysPro-GlyLysCysProValThrTyrglyGlnCysLeuMe 98
Db 347 CNAANCCCAACAAGNGNAACCTTGGNAAGTNCNAGTANTTNGCCCAATGTTNGAT 288
Qy 98 tLeuAsnProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCy 118
Db 287 GCTNAACCCCCCAATTTCTGTGAGATGGATGGCCAGTGCACGCGTGAAGTGTG 228
Qy 118 sMetGlyMetCysGlyLysSerCysValSerProValLysAla 132
Db 227 CATGGGCATGTGTGGGAAATCTCGCTTCCCTGTGAAAGCT 185

RESULT 39
US-09-873-319-9/c
; Sequence 9, Application US/09873319A
; Publication No. US20030134324A1
; GENERAL INFORMATION:
; APPLICANT: Munger, William E.
; APPLICANT: Kulkarni, Prakash
; APPLICANT: Getzenberg, Robert H.
; APPLICANT: Waga, Iwao
; APPLICANT: Yamamoto, Jun
; TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplasia
; FILE REFERENCE: 44921-5029-US
; CURRENT APPLICATION NUMBER: US/09/873,319A
; CURRENT FILING DATE: 2001-06-05
; EARLIER APPLICATION NUMBER: US 60/223,323
; EARLIER FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 755
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 411
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(411)
; OTHER INFORMATION: n = a or c or g or t
US-09-873-319-9

Alignment Scores:
Pred. No.: 1,66e-22 Length: 411
Score: 264.00 Matches: 53
Percent Similarity: 74.67% Conservative: 3
Best Local Similarity: 70.67% Mismatches: 17
Query Match: 34.65% Indels: 3
DB: 10 Gaps: 1

US-10-613-105-2 (1-132) x US-09-873-319-9 (1-411)
Qy 60 LysLysArgCysCysProAspThrCysGlyIleLysCysLeuAspProValAspThrPro 79
Db 406 AAAAGAAATNTTGGCCNGAAACTTGGNGCATNAANTGCCG-GGNCCTCTGTNNACCCC 348
Qy 80 ---AsnProThrArgArgLysPro-GlyLysCysProValThrTyrglyGlnCysLeuMe 98
Db 347 CNAANCCCAACAAGNGNAACCTTGGNAAGTNCNAGTANTTNGCCCAATGTTNGAT 288
Qy 98 tLeuAsnProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCy 118
Db 287 GCTNAACCCCCCAATTTCTGTGAGATGGATGGCCAGTGCACGCGTGAAGTGTG 228
Qy 118 sMetGlyMetCysGlyLysSerCysValSerProValLysAla 132
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US-10-613-105-2 (1-132) x US-09-960-706-16 (1-411)
Qy 60 LysLysArgCysCysProAspThrCysGlyIleLysCysLeuAspProValAspThrPro 79
Db 406 AAAAGAAATNTTGGCCNGAAACTTGGNGCATNAANTGCCG-GGNCCTCTGTNNACCCC 348
Qy 80 ---AsnProThrArgArgLysPro-GlyLysCysProValThrTyrglyGlnCysLeuMe 98
Db 347 CNAANCCCAACAAGNGNAACCTTGGNAAGTNCNAGTANTTNGCCCAATGTTNGAT 288
Qy 98 tLeuAsnProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCy 118
Db 287 GCTNAACCCCCCAATTTCTGTGAGATGGATGGCCAGTGCACGCGTGAAGTGTG 228
Qy 118 sMetGlyMetCysGlyLysSerCysValSerProValLysAla 132
Db 227 CATGGGCATGTGTGGGAAATCTCGCTTCCCTGTGAAAGCT 185

RESULT 39
US-09-873-319-9/c
; Sequence 9, Application US/09873319A
; Publication No. US20030134324A1
; GENERAL INFORMATION:
; APPLICANT: Munger, William E.
; APPLICANT: Kulkarni, Prakash
; APPLICANT: Getzenberg, Robert H.
; APPLICANT: Waga, Iwao
; APPLICANT: Yamamoto, Jun
; TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplasia
; FILE REFERENCE: 44921-5029-US
; CURRENT APPLICATION NUMBER: US/09/873,319A
; CURRENT FILING DATE: 2001-06-05
; EARLIER APPLICATION NUMBER: US 60/223,323
; EARLIER FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 755
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 411
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(411)
; OTHER INFORMATION: n = a or c or g or t
US-09-873-319-9

Alignment Scores:
Pred. No.: 1,66e-22 Length: 411
Score: 264.00 Matches: 53
Percent Similarity: 74.67% Conservative: 3
Best Local Similarity: 70.67% Mismatches: 17
Query Match: 34.65% Indels: 3
DB: 10 Gaps: 1

US-10-613-105-2 (1-132) x US-09-873-319-9 (1-411)
Qy 60 LysLysArgCysCysProAspThrCysGlyIleLysCysLeuAspProValAspThrPro 79
Db 406 AAAAGAAATNTTGGCCNGAAACTTGGNGCATNAANTGCCG-GGNCCTCTGTNNACCCC 348
Qy 80 ---AsnProThrArgArgLysPro-GlyLysCysProValThrTyrglyGlnCysLeuMe 98
Db 347 CNAANCCCAACAAGNGNAACCTTGGNAAGTNCNAGTANTTNGCCCAATGTTNGAT 288
Qy 98 tLeuAsnProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCy 118
Db 287 GCTNAACCCCCCAATTTCTGTGAGATGGATGGCCAGTGCACGCGTGAAGTGTG 228
Qy 118 sMetGlyMetCysGlyLysSerCysValSerProValLysAla 132
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[illegible]

Qy	95	GlnCysLeuMetLeuAsnProProAsnPheCysGluMetAspGlyGlnCysLysArgAsp	114
Db	1	CAATGTTTGATGCTTAACCCCCCAATTCTGTGAGATGGATGCCAGTCCAAGCGTGAC	60
Qy	115	LeuLysCysCysMetGlyMetCysGlyLysSerCysValSerProValLysAla	132
Db	61	TTGAAGTGTTCATGGGCATGTGTGGGAAATCCTTCGCTTCCCTGTGAAAGCT	114

Search completed: October 24, 2004, 06:01:17
Job time : 452 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 24, 2004, 03:59:24 ; Search time 86 Seconds
(without alignments)

1090.978 Million cell updates/sec

Title: US-10-613-105-2

Perfect score: 762

Sequence: 1 MKSSGUPFLVLALGTLAP.....RDLKCMGKSCVSPVKA 132

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANSHUMAN=0.cdi
-LIST=100 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=45
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-USER=US10613105 @CGN 1.1 69 @runat 22102004 170441 18710 -NCPUS=6 -ICPU=3
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	762	100.0	594	4	US-09-016-434-1271
2	458	60.1	325	4	US-09-016-434-1024
3	348	45.7	194	2	US-07-963-538B-5
4	339	44.5	180	3	US-08-483-503A-2
5	224	29.4	292	4	US-09-404-879A-377
6	224	29.4	292	4	US-09-667-857-377
7	165.5	21.7	515	4	US-09-513-999C-3787
8	165.5	21.7	643	4	US-10-000-489-41
9	156	20.5	321	1	US-08-322-742-11
10	152.5	20.0	478	4	US-09-023-655-1233
11	149.5	19.6	453	4	US-09-621-976-1373
12	149.5	19.6	478	4	US-09-244-111-11

13	149	19.6	571	1	US-08-322-742-14	Sequence 14, Appl
14	149	19.6	2309	4	US-09-016-434-1249	Sequence 149, Ap
15	146	19.2	93	1	US-08-304-051-15	Sequence 15, Appl
16	146	19.2	93	1	US-08-304-051-16	Sequence 16, Appl
17	146	19.2	93	5	PCT-US95-11445-15	Sequence 15, Appl
18	146	19.2	93	5	PCT-US95-11445-16	Sequence 16, Appl
19	140	18.4	177	1	US-08-379-437-3	Sequence 3, Appl
20	140	18.4	234	1	US-09-016-434-673	Sequence 673, App
21	139	18.2	177	1	US-08-379-437-5	Sequence 5, Appl
22	139	18.2	177	1	US-08-379-437-7	Sequence 7, Appl
23	134	17.6	68	2	US-07-963-538B-34	Sequence 34, Appl
24	133.5	17.5	724	3	US-09-724-864-23	Sequence 23, Appl
25	129.5	17.0	449	4	US-09-621-976-19119	Sequence 19119, A
26	129	16.9	67	2	US-07-963-538B-33	Sequence 33, Appl
27	129	16.9	80	1	US-08-304-051-7	Sequence 7, Appl
28	129	16.9	80	1	PCT-US95-11445-11	Sequence 11, Appl
29	129	16.9	80	5	PCT-US95-11445-7	Sequence 7, Appl
30	129	16.9	80	5	PCT-US95-11445-11	Sequence 11, Appl
31	125	16.4	66	2	US-07-963-538B-32	Sequence 32, Appl
32	124	16.3	63	2	US-07-963-538B-31	Sequence 31, Appl
33	124	16.3	89	1	US-08-304-051-12	Sequence 12, Appl
34	124	16.3	89	1	US-08-304-051-13	Sequence 13, Appl
35	124	16.3	89	5	PCT-US95-11445-12	Sequence 12, Appl
36	124	16.3	89	5	PCT-US95-11445-13	Sequence 13, Appl
37	117.5	15.4	753	4	US-09-152-060-34	Sequence 34, Appl
38	112.5	14.8	472	4	US-09-270-767-1693	Sequence 1693, Ap
39	112.5	14.8	472	4	US-09-270-767-16975	Sequence 16975, A
40	112.5	14.8	783	4	US-09-152-060-50	Sequence 50, Appl
41	109.5	14.4	437	3	US-09-383-586-29	Sequence 29, Appl
42	109.5	14.4	437	4	US-09-823-038A-29	Sequence 29, Appl
43	109	14.3	4905	1	US-07-978-895-3	Sequence 3, Appl
44	109	14.3	4905	1	US-08-473-119-3	Sequence 3, Appl
45	109	14.3	4905	2	US-08-475-352-3	Sequence 3, Appl
46	109	14.3	4905	4	US-09-170-699-3	Sequence 3, Appl
47	109	14.3	4975	3	US-09-630-706-3	Sequence 3, Appl
48	109	14.3	5687	4	US-09-919-039-268	Sequence 268, App
49	107.5	14.1	4157	2	US-08-162-146-2	Sequence 2, Appl
50	107.5	14.1	4157	3	US-09-314-127-2	Sequence 2, Appl
51	106	13.9	854	4	US-09-312-283C-365	Sequence 365, App
52	104	13.6	1366	2	US-08-761-248B-3	Sequence 3, Appl
53	101.5	13.3	2365	3	US-09-249-697A-5	Sequence 5, Appl
54	101.5	13.3	2365	3	US-09-363-316B-5	Sequence 5, Appl
55	100.5	13.2	3003	4	US-09-307-794A-314	Sequence 314, App
56	100.5	13.2	3003	4	US-09-505-125A-314	Sequence 314, App
57	100.5	13.2	3003	4	US-09-502-775A-314	Sequence 314, App
58	100.5	13.2	3003	4	US-09-906-700-314	Sequence 314, App
59	100.5	13.2	3003	4	US-09-903-603A-314	Sequence 314, App
60	98	12.9	1042	2	US-08-761-248B-5	Sequence 5, Appl
61	98	12.9	1071	2	US-08-761-248B-1	Sequence 1, Appl
62	97	12.7	4545	6	5183884-3	Patent No. 5183884
63	95.5	12.5	567	4	US-09-489-039A-51	Sequence 51, Appl
64	94.5	12.4	683	4	US-09-799-451-908	Sequence 908, App
65	94.5	12.4	6677	3	US-08-939-366-27	Sequence 27, Appl
66	94.5	12.4	6677	3	US-09-467-997-6	Sequence 6, Appl
67	94.5	12.4	13842	3	US-09-105-537-30	Sequence 30, Appl
68	94.5	12.4	36778	3	US-09-105-537-5	Sequence 5, Appl
69	94.5	12.4	38506	3	US-09-320-878-19	Sequence 19, Appl
70	94.5	12.4	38506	4	US-09-141-908-1	Sequence 1, Appl
71	94.5	12.4	38506	4	US-09-657-440-19	Sequence 19, Appl
72	94	12.3	319	4	US-07-757-022B-55	Sequence 55, Appl
73	94	12.3	390	4	US-07-757-022B-85	Sequence 85, Appl
74	94	12.3	393	4	US-07-757-022B-77	Sequence 77, Appl
75	94	12.3	417	4	US-07-757-022B-33	Sequence 33, Appl
76	94	12.3	423	4	US-07-757-022B-79	Sequence 79, Appl
77	94	12.3	468	4	US-07-757-022B-105	Sequence 105, App
78	94	12.3	469	4	US-07-757-022B-117	Sequence 117, App
79	94	12.3	471	4	US-07-757-022B-101	Sequence 101, App
80	94	12.3	471	4	US-07-757-022B-113	Sequence 113, App
81	94	12.3	516	4	US-07-757-022B-87	Sequence 87, Appl
82	94	12.3	567	4	US-07-757-022B-31	Sequence 31, Appl
83	94	12.3	576	4	US-07-757-022B-89	Sequence 89, Appl
84	94	12.3	612	4	US-07-757-022B-91	Sequence 91, Appl
85	94	12.3	621	4	US-07-757-022B-115	Sequence 115, App

Sequence 135, App
Sequence 131, App
Sequence 93, App1
Sequence 95, App1
Sequence 29, App1
Sequence 29, App1
Sequence 69, App1
Sequence 357, App
Sequence 53, App1
Sequence 103, App
Sequence 41, App1
Sequence 47, App1
Sequence 39, App1
Sequence 61, App1
Sequence 1, App1

86 94 12.3 621 4 US-07-757-022B-135
87 94 12.3 624 4 US-07-757-022B-131
88 94 12.3 627 4 US-07-757-022B-93
89 94 12.3 660 4 US-07-757-022B-95
90 94 12.3 696 4 US-07-757-022B-29
91 94 12.3 714 4 US-07-757-022B-71
92 94 12.3 891 4 US-07-757-022B-69
93 94 12.3 1206 4 US-09-312-283C-357
94 12.3 1392 4 US-07-757-022B-53
95 94 12.3 3420 4 US-07-757-022B-103
96 94 12.3 3936 4 US-07-757-022B-41
97 94 12.3 4065 4 US-07-757-022B-47
98 94 12.3 4086 4 US-07-757-022B-39
99 94 12.3 4215 4 US-07-757-022B-61
100 94 12.3 5008 4 US-07-757-022B-1

ALIGNMENTS

RESULT 1

US-09-016-434-1271
; Sequence 1271, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1271:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 594 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g28638
; US-09-016-434-1271

Alignment Scores:
Pred. No.: 4.21e-72 Length: 594
Score: 762.00 Matches: 132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

DB: 4 Gaps: 0
US-10-613-105-2 (1-132) x US-09-016-434-1271 (1-594)

QY 1 MetLysSerSerGlyLeuPheProPheLeuValLeuLeuAlaLeuGlyThrLeuAlaPro 20
Db 19 ATGAAGTCAGCGGCCCTCTTCCTCCCTTCCCTGGTCTCTGGGAACTCTGGCACCT 78
QY 21 TtAlaValGlyGlySerGlyLysSerPheLysAlaGlyValCysProLysLysSer 40
Db 79 TGGGCTGTGGAAGCTCTGGAAGTCTTCAAGAGCTGGAGTCTGTCTCTCTAAGAAATCT 138
QY 41 AlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAspTropGlnCysProGlyLys 60
Db 139 GCCCAGTCTCTAGATACAAAGAAACCTGAGTGCAGAGTACTGGCAGTGTCCAGGGAAG 198
QY 61 LysArgCysCysProAspThrCysGlyLysCysLeuAspProValAspThrProAsn 80
Db 199 AAGAGATGTGTCTCTGACACTTGTGGCATCAATGCTGGATCCTGTTGACACCCCAAC 258
QY 81 ProThrArgArgLysProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAsn 100
Db 259 CCNACCAAGAGGAGGAGCTGGGAGTCCAGAGTACTATGGCCAAATGTTGATGCTTAAC 318
QY 101 ProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGly 120
Db 319 CCCCCCAATTTCTGTGAGATGGATGCCAGTGCCAGTGTGAAGTGTTCATGGGCGC 378
QY 121 MetCysGlyLysSerCysValSerProValLysAla 132
Db 379 ATGTGTGGGAAATCTCGCTTTCCCTGTGAAAGCT 414

RESULT 2

US-09-016-434-1024
; Sequence 1024, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1024:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 base pairs
; TYPE: nucleic acid

RESULT 9
US-08-322-742-11
; Sequence 11, Application US/08322742
; Patent No. 5688641
; GENERAL INFORMATION:
; APPLICANT: Sager, Ruth
; TITLE OF INVENTION: CANCER DIAGNOSIS AND THERAPY
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/322,742
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/938,823
; FILING DATE: September 1, 1992
; APPLICATION NUMBER: 07/844,296
; FILING DATE: February 28, 1992
; APPLICATION NUMBER: 07/552,216
; FILING DATE: February 28, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00530/048003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 321
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-322-742-11
Alignment Scores:
Pred. No.: 4.25e-08 Length: 321
Score: 156.00 Matches: 33
Percent Similarity: 39.78% Conservative: 4
Best Local Similarity: 35.48% Mismatches: 36
Query Match: 20.47% Indels: 20
DB: 1 Gaps: 2
US-10-613-105-2 (1-132) x US-08-322-742-11 (1-321)
Qy 57 CysProGly-----LysLysArgCysCysProAspThrCysGlyIleLysCys 72
Db 33 TGTACGGGGAGTTCCTGTTAAAGGTCAAGACCCCTGTCAAAGCGCGTGTTCATCAATGGA 92
Qy 73 LeuAspProVal----- 76
Db 93 CAAGATCCCGTTAAAGGACAAGTTTCAGTTAAAGGTCAAGTAAAGTCAAGCGCAAGAG 152
Qy 77 AspThrProAsnProThrArgArgLysProGlyLysCysProValThrTyrGlyGlnCys 96
Db 153 CCAGTCAAAGGTCAGTCTCCACTAAGCTGGCTCTGCTGCCCATATCTTGTATCCGGTGC 212
Qy 97 LeuMetLeuAsnProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLys 116
Db 213 GCCATGTGTAATCTCTCAACCGCTGCTTGAAGATACTGACTGCCGCCAGGAATCAAGAAG 272
Qy 117 CysCysMetGlyMetCysGlyLysSerCysValSerPro 129

Db 273 TGCTGTGAAGCTCTTGGCGGATGGCTGTTTCGTTCCC 311
RESULT 10
US-09-023-655-1233
; Sequence 1233, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1233:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g28711
US-09-023-655-1233
Alignment Scores:
Pred. No.: 1.74e-07 Length: 478
Score: 152.50 Matches: 47
Percent Similarity: 41.48% Conservative: 9
Best Local Similarity: 34.81% Mismatches: 55
Query Match: 20.01% Indels: 25
DB: 4 Gaps: 5
US-10-613-105-2 (1-132) x US-09-023-655-1233 (1-478)
Qy 1 MetLysSerSerGlyLeuPheProPheLeuValLeuAlaLeuGlyThrLeuAla--- 19
Db 3 ATAGGCGCAGCAGCTTCTTGATCGTGGTGGTTCCTCATCGCTGGACGCTGGTTCTA 62
Qy 20 ProTrpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProProLysLys 39
Db 63 GAGGCAGCTGTACGGGA-----GTTCCTGTTAAAGG- 94
Qy 40 SerAlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAspTrp-GlnCysProGl 59
Db 95 TCAAGACACTGTCAAAGG-----CCGTGTTCCATTCAATGGACAAGATCCCGT 142

STREET: 225 Franklin Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: U.S.A.
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 COMPUTER: IBM PS/2 Model 50Z or 55SX
 OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
 SOFTWARE: WordPerfect (Version 5.1)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/322,742
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/938,823
 FILING DATE: September 1, 1992
 APPLICATION NUMBER: 07/844,296
 FILING DATE: February 28, 1992
 APPLICATION NUMBER: 07/552,216
 FILING DATE: February 28, 1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Fraser, Janis K.
 REGISTRATION NUMBER: 34,819
 REFERENCE/DOCKET NUMBER: 00530/048003
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-5070
 TELEFAX: (617) 542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 571
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 US-08-322-742-14

Alignment Scores:
 Pred. No.: 5,25e-07 Length: 571
 Score: 149.00 Matches: 28
 Percent Similarity: 55.00% Conservative: 5
 Best Local Similarity: 46.67% Mismatches: 25
 Query Match: 19.55% Indels: 2
 DB: 1 Gaps: 1

US-10-613-105-2 (1-132) x US-08-322-742-14 (1-571)

QY 70 IleLysCysLeuAspProValAspThrProAsnProThrArgArgLysProGlyLysCys 89
 Db 193 GTCAAGCGCAAGAGCCAGTCAAGGTCAGTCTCCACT-----AAGCCTGGCTCCTGC 246
 QY 90 ProValThrTyrglyGlnCysLeuMetLeuAsnProProAsnPheCysGluMetAspGly 109
 Db 247 CCATTATCTTGTATCGCGTGGCCATGTTGAATCTCTTAACCGCTGCTTGAAGATACT 306
 QY 110 GlnCysLysArgAspLeuLysCysMetCysGlyMetCysGlyLysSerCysValSerPro 129
 Db 307 GACTGCCAGGAATCAAGAAGTCTGTGAAGGCTCTTGGCGGATGGCTGTTTCGTCCC 366

RESULT 14

US-09-016-434-1249
 ; Sequence 1249, Application US/09016434
 ; Patent No. 6500938

GENERAL INFORMATION:
 ; APPLICANT: Janice Au-Young
 ; APPLICANT: Jeffrey J. Sellhamer
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
 ; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
 ; NUMBER OF SEQUENCES: 1490
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 ; STREET: 3174 PORTER DRIVE
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA

COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/016,434
 FILING DATE: HERewith
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Zeller, Karen J.
 REGISTRATION NUMBER: 37,071
 REFERENCE/DOCKET NUMBER: PA-0002 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 855-0555
 TELEFAX: (650) 845-4166
 INFORMATION FOR SEQ ID NO: 1249:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2309 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GENBANK
 CLONE: g190337
 US-09-016-434-1249

Alignment Scores:
 Pred. No.: 3,67e-06 Length: 2309
 Score: 149.00 Matches: 38
 Percent Similarity: 43.97% Conservative: 13
 Best Local Similarity: 32.76% Mismatches: 52
 Query Match: 19.55% Indels: 13
 DB: 4 Gaps: 4

US-10-613-105-2 (1-132) x US-09-016-434-1249 (1-2309)

QY 21 TrpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProProLysLysSer 40
 Db 1394 TGCACCTGAAGCAGAGGCTTACTGGGTATTAATGTGGGCTCGTTCTTTTAAACAGT 1453
 QY 41 AlaGlnCys-----LeuArgTyrlsLysProGluCysGlnSerAspTrp-GlnCysPr 58
 Db 1454 TCC---TGTTAAAGGTCAAGACACTGTCAAAGCCGCTGTTCATTCAATGGACAAGATCC 1510
 QY 58 oGlyLysLysArgCysCysProAspThrCysGlyLleLysCysLeuAspProValAspTh 78
 Db 1511 CGTTAAAGACAA-----GTTTCAGTTAAAGGTCAAGATCAAGTCAAGC 1555
 QY 78 rProAsnProThrArg-----ArgLysProGlyLysCysProValThrTyrl 94
 Db 1556 GCAAGAGCCAGTCAAGGTCAGTCTCCACTAAGCTTGGCTCTGCCCATTTATTTGAT 1615
 QY 94 yGlnCysLeuMetLeuAsnProProAsnPheCysGluMetAspGlyGlnCysLysArgAs 114
 Db 1616 CCGGTGGCCATGTTGAATCCCCCTAACCGCTCTTTGAAAGATACTGACTGCCCGGAAT 1675
 QY 114 pLeuLysCysCysMetGlyMetCysGlyLysSerCysValSerPro 129
 Db 1676 CAAGAAGTCTGTGAAGGCTCTTTCGGGATGGCTGTTTCGTTCCC 1721

RESULT 15

US-08-304-051-15
 ; Sequence 15, Application US/08304051
 ; Patent No. 5633227

GENERAL INFORMATION:
 ; APPLICANT: Muller, Daniel K.; Brownell, Elise; Delaria, Katherine A.

; TITLE OF INVENTION: Secretory Leukocyte Protease Inhibitor as an
; TITLE OF INVENTION: Inhibitor of Trypsin
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Miles Inc.
; STREET: 400 Morgan Lane
; CITY: West Haven
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06516
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1,300 Kb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word Perfect 3.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/304,051
; FILING DATE: 12-Sept-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA: No. 5633227e
; ATTORNEY/AGENT INFORMATION:
; NAME: William F. Gray
; REGISTRATION NUMBER: 31018
; REFERENCE/DOCKET NUMBER: MWH 322
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203) 937-2712
; TELEFAX: (203) 937-2795
; TELEX: 221949 MILES UR
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 93 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: - Other nucleic Acid: synthetic
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: Primer for Polymerase Chain Reaction used to make mutein
; US-08-304-051-15
Alignment Scores:
Pred. No.: 8.76e-08 Length: 93
Score: 146.00 Matches: 26
Percent Similarity: 96.30% Conservative: 0
Best Local Similarity: 96.30% Mismatches: 1
Query Match: 19.16% Indels: 0
DB: 1 Gaps: 0
US-10-613-105-2 (1-132) x US-08-304-051-15 (1-93)
Qy 25 GlySerGlyLysSerPheLysAlaGlyValCysProProLysLysSerAlaGlnCysLeu 44
Db 12 GGCTCTGGAAGTCTTCAAGCTGGAGTGTCTCTTAAGAAATCTGCCAGTGCAGA 71
Qy 45 ArgTyrLysLysProGluCys 51
Db 72 AGATACAAAGAACTGAGTGC 92
RESULT 16
US-08-304-051-16
; Sequence 16, Application US/08304051
; Patent No. 5633227
; GENERAL INFORMATION:
; APPLICANT: Muller, Daniel K.; Brownell, Elise; Delaria, Katherine A.
; TITLE OF INVENTION: Secretory Leukocyte Protease Inhibitor as an
; TITLE OF INVENTION: Inhibitor of Trypsin
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Miles Inc.
; STREET: 400 Morgan Lane

; CITY: West Haven
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06516
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1,300 Kb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word Perfect 3.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/304,051
; FILING DATE: 12-Sept-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA: No. 5633227e
; ATTORNEY/AGENT INFORMATION:
; NAME: William F. Gray
; REGISTRATION NUMBER: 31018
; REFERENCE/DOCKET NUMBER: MWH 322
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203) 937-2712
; TELEFAX: (203) 937-2795
; TELEX: 221949 MILES UR
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 93 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: - Other nucleic Acid: synthetic
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: Primer for Polymerase Chain Reaction used to make mutein
; US-08-304-051-16
Alignment Scores:
Pred. No.: 8.76e-08 Length: 93
Score: 146.00 Matches: 26
Percent Similarity: 96.30% Conservative: 0
Best Local Similarity: 96.30% Mismatches: 1
Query Match: 19.16% Indels: 0
DB: 1 Gaps: 0
US-10-613-105-2 (1-132) x US-08-304-051-16 (1-93)
Qy 25 GlySerGlyLysSerPheLysAlaGlyValCysProProLysLysSerAlaGlnCysLeu 44
Db 12 GGCTCTGGAAGTCTTCAAGCTGGAGTGTCTCTTAAGAAATCTGCCAGTGCAGA 71
Qy 45 ArgTyrLysLysProGluCys 51
Db 72 AGATACAAAGAACTGAGTGC 92
RESULT 17
PCT-US95-11445-15
; Sequence 15, Application PC/TUS9511445
; GENERAL INFORMATION:
; APPLICANT: Muller, Daniel K.; Brownell, Elise; Delaria,
; APPLICANT: Katherine A.
; TITLE OF INVENTION: Secretory Leukocyte Protease
; TITLE OF INVENTION: Inhibitor as an Inhibitor of Trypsin
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bayer Corporation
; STREET: 400 Morgan Lane
; CITY: West Haven
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06516
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1,300 Kb storage


```

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 673:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 234 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LONGTUT09
; CLONE: 2657496
; US-09-016-434-673

Alignment Scores:
Pred. No.: 1.37e-06 Length: 234
Score: 140.00 Matches: 32
Percent Similarity: 55.84% Conservative: 11
Best Local Similarity: 41.56% Mismatches: 30
Query Match: 18.37% Indels: 4
DB: 3

US-10-613-105-2 (1-132) x US-09-016-434-673 (1-234)

Qy 1 MetLysSerSerGlyLeuPheProPheLeuValLeuLeuAlaLeuGlyThrLeuAlaPro 20
Db 5 ATGGGGTCCAGCAGCTTCTTGGTCTCATGTGTCTCTCGTTCTGTGACCCCTGGTG--- 61
Qy 21 TrpAlaValGluGlySerGlyLysSerPhe---LysAlaGlyValCysProProLysLys 39
Db 62 ---GCTGTGAAGAGGATTAAAGAGGGATAGAGAAAGCAGGGGTTTC---CCAGCTGAC 115
Qy 40 SerAlaGlnCysLeuArgTyLysLysProGluCysGlnSerAspTrpGlnCysProGly 59
Db 116 AACGTACCGTGTCTTCAAGTCGCGATCTCTCCAGTGTGCACAGACCAGGAGCTGTCTGGG 175
Qy 60 LysLysAspGlyCysProAspThrCysGlyIleLysCysLeuAspProVal 76
Db 176 GAAAGGAGTGTGTACTGCACCTGTGGCTTCAAGTGTGTGATTCCTGTG 226

RESULT 21
US-08-379-437-5
; Sequence 5, Application US/08379437
; Patent No. 5734014
; GENERAL INFORMATION:
; APPLICANT: ISHIMA, YOSHIKI
; APPLICANT: OKAWA, NORIYUKI
; APPLICANT: YOSHIDA, MASAYA
; APPLICANT: AMAGAYA, SAKAE
; APPLICANT: KAJI, AKIRA
; TITLE OF INVENTION: NOVEL ELAFIN DERIVATIVE
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
; STREET: 1755 S. JEFFERSON DAVIS HWY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30

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/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/379,437
/ FILING DATE: 27-MAR-1995
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: JP PCT/JP93/01133
/ FILING DATE: 11-AUG-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: JP PCT/JP93/01133
/ FILING DATE: 11-AUG-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: OBLON, NORMAN F
/ REGISTRATION NUMBER: 24,618
/ TELEPHONE: 703-413-3000
/ TELEFAX: 703-413-2220
/ TELEX: 248855 OPAT UR
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 177 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: other nucleic acid
/ DESCRIPTION: /desc = "synthetic DNA"
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1..171
/
/ US-08-379-437-5
/
Alignment Scores:
Pred. No.: 1.19e-06 Length: 177
Score: 139.00 Matches: 26
Percent Similarity: 55.36% Conservative: 5
Best Local Similarity: 46.43% Mismatches: 23
Query Match: 18.24% Indels: 2
DB: 1 Gaps: 1
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US-10-613-105-2 (1-132) x US-08-379-437-5 (1-177)
/
QY 74 AspProValAspThrProAsnProThrArgArgLysProGlyLysCysProValThrTyr 93
Db 7 GAACCAAGTTAAAGTCCGGTGTGCGACC-----AAACCGGGCTCTTGGCCGATTATCCTG 60
/
QY 94 GlyGlnCysLeuMetLeuAsnProAsnPheCysGluMetAspGlyGlnCysLysArg 113
Db 61 ATCCGCTGCGCTGTCTGAACCGCCGCAACCGTTGTCTGAAAGACACTGACTGCCCGGGT 120
/
QY 114 AspLeuLysCysCysMetGlyMetCysGlyLysSerCysValSerPro 129
Db 121 ATCAAAAATGCTGCGAAGGTTCTTGGCGGTATGGCATGCTTCGTTCCG 168
/
RESULT 22
US-08-379-437-7
/ Sequence 7, Application US/08379437
/ Patent No. 5734014
/ GENERAL INFORMATION:
/ APPLICANT: ISHIMA, YOSHIAKI
/ APPLICANT: OKAWA, NORIYUKI
/ APPLICANT: YOSHIDA, MASAYA
/ APPLICANT: AMAGAWA, SAKAE
/ APPLICANT: KAJI, AKIRA
/ TITLE OF INVENTION: NOVEL ELAFIN DERIVATIVE
/ NUMBER OF SEQUENCES: 16
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
/ STREET: 1755 S. JEFFERSON DAVIS HWY, SUITE 400
/ CITY: ARLINGTON
/ STATE: VA
/ COUNTRY: USA
/ ZIP: 22202
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/
/
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/379,437
/ FILING DATE: 27-MAR-1995
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: JP PCT/JP93/01133
/ FILING DATE: 11-AUG-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: OBLON, NORMAN F
/ REGISTRATION NUMBER: 24,618
/ TELEPHONE: 703-413-3000
/ TELEFAX: 703-413-2220
/ TELEX: 248855 OPAT UR
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 177 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: other nucleic acid
/ DESCRIPTION: /desc = "synthetic DNA"
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1..171
/
/ US-08-379-437-7
/
Alignment Scores:
Pred. No.: 1.19e-06 Length: 177
Score: 139.00 Matches: 26
Percent Similarity: 55.36% Conservative: 5
Best Local Similarity: 46.43% Mismatches: 23
Query Match: 18.24% Indels: 2
DB: 1 Gaps: 1
/
US-10-613-105-2 (1-132) x US-08-379-437-7 (1-177)
/
QY 74 AspProValAspThrProAsnProThrArgArgLysProGlyLysCysProValThrTyr 93
Db 7 GAACCAAGTTAAAGTCCGGTGTGCGACC-----AAACCGGGCTCTTGGCCGATTATCCTG 60
/
QY 94 GlyGlnCysLeuMetLeuAsnProAsnPheCysGluMetAspGlyGlnCysLysArg 113
Db 61 ATCCGCTGCGCTGTCTGAACCGCCGCAACCGTTGTCTGAAAGACACTGACTGCCCGGGT 120
/
QY 114 AspLeuLysCysCysMetGlyMetCysGlyLysSerCysValSerPro 129
Db 121 ATCAAAAATGCTGCGAAGGTTCTTGGCGGTATGGCATGCTTCGTTCCG 168
/
RESULT 23
US-07-963-5388-34/c
/ Sequence 34, Application US/079635388
/ Patent No. 5851983
/ GENERAL INFORMATION:
/ APPLICANT: SUGIYAMA, TAKASHI
/ APPLICANT: KAMIMURA, TAKASHI
/ APPLICANT: MASUDA, KENICHI
/ APPLICANT: OKADA, MASAHIRO
/ APPLICANT: OHTSUKA, EIKO
/ APPLICANT: IMAIZUMI, ATSUSHI
/ APPLICANT: WATANABE, KUNIHITO
/ APPLICANT: SUGA, TETSUYA
/ APPLICANT: MATSUMOTO, YOHICHI
/ APPLICANT: TAKEUCHI, AKIO
/ TITLE OF INVENTION: ELASTASE INHIBITORY POLYPEPTIDE AND
/ PROCESS FOR PRODUCTION THEREOF BY RECOMBINANT GENE
/ TITLE OF INVENTION: TECHNOLOGY
```

; NUMBER OF SEQUENCES: 36
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: COOLEY GODWARD LLP
 ; STREET: FIVE PALO ALTO SQUARE, 4TH FLOOR
 ; CITY: PALO ALTO
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94306-2155
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/963,538B
 ; FILING DATE: 20-OCT-1992
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/843,359
 ; FILING DATE: 25-FEB-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/408,483
 ; FILING DATE: 22-AUG-1989
 ; PRIOR APPLICATION DATA: JP 4-212399
 ; FILING DATE: 17-JUL-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 4-212398
 ; FILING DATE: 17-JUL-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 3-355553
 ; FILING DATE: 24-DEC-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 62-330219
 ; FILING DATE: 28-DEC-1987
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: NEELEY PH.D., RICHARD L.
 ; REGISTRATION NUMBER: 30,092
 ; REFERENCE/DOCKET NUMBER: TEJN-005/02US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-843-5070
 ; TELEFAX: 415-857-0663
 ; TELEX: 380816 COOLEY PA
 ; INFORMATION FOR SEQ ID NO: 34:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 68 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single stranded
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (synthetic)
 ; US-07-963-538B-34

Alignment Scores:
 Pred. No.: 1,07e-06 Length: 68
 Score: 134.00 Matches: 22
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 17.59% Indels: 0
 DB: 2 Gaps: 0

US-10-613-105-2 (1-132) x US-07-963-538B-34 (1-68)

Qy 98 MetLeuAsnProAsnPheCysGluMetAspGlyGlnCysLysAtgAspLeuLysCys 117
 Db 66 ATGCTGAACCCGCGCACTTCTGTGAATATGACGGTCAGTGTAAACGAGATCTGAATGT 7
 Qy 118 CysMet 119
 Db 6 TGTATG 1

RESULT 24

US-09-724-864-23

; Sequence 23, Application US/09724864

; Patent No. 6380362
 ; GENERAL INFORMATION:
 ; APPLICANT: Watson, James D.
 ; APPLICANT: Murison, James G.
 ; TITLE OF INVENTION: Polynucleotides, polypeptides expressed
 ; TITLE OF INVENTION: by the polynucleotides and methods for their use.
 ; FILE REFERENCE: 11000.1050U1
 ; CURRENT APPLICATION NUMBER: US/09/724,864
 ; PRIOR FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: U.S. NO. 6380362 60/171,678
 ; PRIOR FILING DATE: 1999-12-23
 ; NUMBER OF SEQ ID NOS: 72
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 23
 ; LENGTH: 724
 ; TYPE: DNA
 ; ORGANISM: Mouse
 ; US-09-724-864-23

Alignment Scores:
 Pred. No.: 3.24e-05 Length: 724
 Score: 133.50 Matches: 44
 Percent Similarity: 32.20% Conservative: 13
 Best Local Similarity: 24.86% Mismatches: 53
 Query Match: 17.52% Indels: 67
 DB: 3 Gaps: 9

US-10-613-105-2 (1-132) x US-09-724-864-23 (1-724)

Qy 10 LeuValLeuLeuAlaLeuGlyThrLeu-----AlaProTtpAlaVal 23
 Db 16 CTCTGCTTGTGGCGCTGCTCTACTAGGTGTTGCTACTTACCCCATCTCAGCC 75
 Qy 24 GluGlySerGlyLysSerPheLysAlaGlyValCysProPro---LysLysSerAlaGln 42
 Db 76 ACAGGCACCGATCGCAGAG---AAACCCGGCGAGTGGCCCGAGCTCGAACCAATTACCGAC 132
 Qy 43 CysLeuArgTyrLysLysProGluCysGlnSerAspTrpGlnCysProGlyLysLysArg 62
 Db 133 TGTGTGTGTG-----GAGTGCATCTTGGACAAGGACTGTGCGGACAAACCGCAAG 180
 Qy 63 CysCysProAspThrCysGlyLleLysCysLeuAspPro----- 75
 Db 181 TGCTGCCAGCGCGGCTGCAGCTCTGTCTGCCAAGCCTAATGACCGAGCGAAGGAGAG 240
 Qy 75 ----- 75
 Db 241 CTCTCAGGACACATATAACTCTCAGAGACTGGGACTACTCAATCAGCGGGCCTT 300
 Qy 76 -----ValAspThrProAsnPro----- 81
 Db 301 GACCACACTACTAAACCCGCGGAGGTCAAGTCTCCACGAAGCCACCGGCTGTGACCAGG 360
 Qy 82 -----ThrArgArgLysProGlyLysCysProValThr-----Tyr 93
 Db 361 GAAGGCTTAGGTGTCGAGAGAAAAGCAGGCGCACCTGCCCCAGCGCTGGACATACCACAGCTC 420
 Qy 94 GlyGlnCysLeuMetLeuAsnProProAsnPheCysGluMetAspGlyGlnCysLysArg 113
 Db 421 GGCCTCTGT-----GAGGACCACTGTGAGGTGACAGCCAGTGTCTTGGC 465
 Qy 114 AspLeuLysCysCysMetGlyMetCysGlyLys---SerCysValSerPro 129
 Db 466 AACATGAATATGCTGCCCAATGATGTGGAGAGATGTCCTGCACACACACCC 516

RESULT 25

US-09-621-976-19119

; Sequence 19119, Application US/09621976

; Patent No. 6639063

; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.

; APPLICANT: Jobert, S.

; APPLICANT: Giordano, J.Y.

; TITLE OF INVENTION: ESTs and Encoded Human Proteins.

; FILE REFERENCE: GENSET.054PR2

; CURRENT APPLICATION NUMBER: US/09/621,976

; CURRENT FILING DATE: 2000-07-21

; NUMBER OF SEQ ID NOS: 19335

; SOFTWARE: Patent.pm

; SEQ ID NO 19119

; LENGTH: 449

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-621-976-19119

Alignment Scores:
Pred. No.: 4 43e-05 Length: 449
Score: 129.50 Matches: 41
Percent Similarity: 34.78% Conservative: 7
Best Local Similarity: 29.71% Mismatches: 41
Query Match: 16.99% Indels: 49
DB: 4 Gaps: 8

US-10-613-105-2 (1-132) x US-09-621-976-19119 (1-449)

QY 31 LysAlaGlyValCysProProLysLysSerAlaGlnCysLeuArgTyrLysLysProGlu 50
DB 54 AAAGAGGAGATGCCCTCCGATAGAAC---CCATGC-----AAAGAGCTG 98
QY 51 CysGlnSerAspTrpGlnCysProGlyLysLysArgCysCysProAspThrCysGlyIle 70
DB 99 TGCAGGGCGCATGAATGTCTCGGCTGAACAGAGAGTGTGCACCAAGCTGTGTCGG 158
QY 71 LysCysLeuAsp---ProValAsp-----77
DB 159 ATCTGCCGAGACATCTCTAAGGACGGATTTGCTCTTGTGCTCAGACTAGATGAGTG 218
QY 78 -----ThrProAsn 80
DB 219 GCGTGATCTCGGCTCACCGCAACCTCTGCTCCGGGTTCAAGTGATTCCTGCTCTCAG 278
QY 81 Pro-----ThrArgArgLysProGlyLysCysPro-----ValThr 92
DB 279 CCTCCCAAGTAGTGGGATTACAGGAGGAAA---AGAGATTGCCCTAGGGTTATTTCGG 335
QY 93 TyrGlyGlnCysLeuMetLeuAsnProProAsnPheCysGluMetAspGlyGlnCysLys 112
DB 336 AAACATCTCTGTTG-----AAAAGTGCATCACTGATGAGACATGTCCA 380
QY 113 ArgAspLeuLysCysCysMetGlyMetCysGlyLysSerCysValSerProVal 130
DB 381 GGTGTAAGAWATGCTGCAGCGCTTGCTGCAACAGAGCTGTGTAGTCCCAATC 434

RESULT 26
US-07-963-538B-33
; Sequence 33, Application US/07963538B
; Patent No. 5851983
; GENERAL INFORMATION:
; APPLICANT: SUGIYAMA, TAKASHI
; APPLICANT: KAMIMURA, TAKASHI
; APPLICANT: MASUDA, KENICHI
; APPLICANT: OKADA, MASAHITO
; APPLICANT: OHTSUKA, EIKO
; APPLICANT: IMAIZUMI, ATSUSHI
; APPLICANT: WATANABE, KUNIHITO
; APPLICANT: SUGA, TETSUYA
; APPLICANT: MATSUMOTO, YOHICHI
; APPLICANT: TAKEUCHI, AKIKO
; TITLE OF INVENTION: ELASTASE INHIBITORY POLYPEPTIDE AND
; TITLE OF INVENTION: PROCESS FOR PRODUCTION THEREOF BY RECOMBINANT GENE
; TITLE OF INVENTION: TECHNOLOGY
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOLEY GODWARD LLP
; STREET: FIVE PALO ALTO SQUARE, 4TH FLOOR
; CITY: PALO ALTO

; STATE: CA
; COUNTRY: USA
; ZIP: 94106-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/963,538B
; FILING DATE: 20-OCT-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/843,359
; FILING DATE: 25-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/408,483
; FILING DATE: 22-AUG-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-212399
; FILING DATE: 17-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-212398
; FILING DATE: 17-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-355553
; FILING DATE: 24-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 62-330219
; FILING DATE: 28-DEC-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: NEELEY PH.D., RICHARD L.
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: TEJN-005/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5070
; TELEFAX: 415-857-0663
; TELEX: 380816 COOLEY PA
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 67 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (synthetic)
US-07-963-538B-33

Alignment Scores:
Pred. No.: 3 55e-06 Length: 67
Score: 129.00 Matches: 22
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 16.93% Indels: 0
DB: 2 Gaps: 0

US-10-613-105-2 (1-132) x US-07-963-538B-33 (1-67)

QY 95 GlnCysLeuMetLeuAsnProProAsnPheCysGluMetAspGlyGlnCysLysArgAsp 114
DB 1 CAGTGTCTGATGCTGAACCGCGCACTTCTGTGAAATGACGCTCAGTGTAAACGAGAT 60
QY 115 LeuLys 116
DB 61 CTGAAA 66

RESULT 27
US-08-304-051-7
; Sequence 7, Application US/08304051
; Patent No. 5633227
; GENERAL INFORMATION:
; APPLICANT: Muller, Daniel K.; Brownell, Elise; Delaria, Katherine A.
; TITLE OF INVENTION: Secretary Leukocyte Protease Inhibitor as an
; TITLE OF INVENTION: Inhibitor of Trypsase

US-10-613-105-2 (1-132) x PCT-US95-11445-11 (1-80)

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US-07-963-538B-32/c
; Sequence 32, Application US/07963538B
; Patent No. 5851983
;
; GENERAL INFORMATION:
; APPLICANT: SUGIYAMA, TAKASHI
; APPLICANT: KAMIMURA, TAKASHI
; APPLICANT: MASUDA, KENICHI
; APPLICANT: OKADA, MASAHIRO
; APPLICANT: OHTSUKA, EIKO
; APPLICANT: IMAIZUMI, ATSUSHI
; APPLICANT: WATANABE, KUNIHITO
; APPLICANT: SUGA, TETSUYA
; APPLICANT: MATSUMOTO, YOHICHI
; APPLICANT: TAKEUCHI, AKIKO
;
; TITLE OF INVENTION: ELASTASE INHIBITORY POLYPEPTIDE AND
; TITLE OF INVENTION: PROCESS FOR PRODUCTION THEREOF BY RECOMBINANT GENE
;
; NUMBER OF SEQUENCES: 36
;
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: COOLEY GODWARD LLP
; STREET: FIVE PALO ALTO SQUARE, 4TH FLOOR
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
;
; ZIP: 94306-2155
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/963,538B
; FILING DATE: 20-OCT-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/843,359
; FILING DATE: 25-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/408,483
; FILING DATE: 22-AUG-1989
; APPLICATION DATA:
; APPLICATION NUMBER: JP 4-212399
; FILING DATE: 17-JUL-1992
; APPLICATION DATA:
; APPLICATION NUMBER: JP 4-212398
; FILING DATE: 17-JUL-1992
; APPLICATION DATA:
; APPLICATION NUMBER: JP 3-355553
; FILING DATE: 24-DEC-1991
; APPLICATION DATA:
; APPLICATION NUMBER: JP 62-330219
; FILING DATE: 28-DEC-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: NEELEY PH.D., RICHARD L.
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: TEJN-005/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5070
; TELEFAX: 415-857-0663
; TELEX: 380816 COOLEY PA
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 66 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (synthetic)
; US-07-963-538B-32

Alignment Scores:
Pred. No.: 9,25e-06 Length: 66
Score: 125.00 Matches: 21
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 16.40% Indels: 0
DB: 2 Gaps: 0

US-10-613-105-2 (1-132) x US-07-963-538B-32 (1-66)

QY 76 ValAspThrProAsnProThrArgArgLysProGlyLysCysProValThrTyrGlyGln 95
Db 64 GTGACACCCCGAACCGACCGTCTGTAAACCGGGTAAATGTCCGGTTACATATGTCAG 5

QY 96 Cys 96
Db 4 TGT 2

RESULT 32
US-07-963-538B-31
; Sequence 31, Application US/07963538B
; Patent No. 5851983
; GENERAL INFORMATION:
; APPLICANT: SUGIYAMA, TAKASHI
; APPLICANT: KAMIMURA, TAKASHI
; APPLICANT: MASUDA, KENICHI
; APPLICANT: OKADA, MASAHIRO
; APPLICANT: OHTSUKA, EIKO
; APPLICANT: IMAIZUMI, ATSUSHI
; APPLICANT: WATANABE, KUNIHITO
; APPLICANT: SUGA, TETSUYA
; APPLICANT: MATSUMOTO, YOHICHI
; APPLICANT: TAKEUCHI, AKIO
```

```
; TITLE OF INVENTION: ELASTASE INHIBITORY POLYPEPTIDE AND
; TITLE OF INVENTION: PROCESS FOR PRODUCTION THEREOF BY RECOMBINANT GENE
; TITLE OF INVENTION: TECHNOLOGY
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOLEY GODWARD LLP
; STREET: FIVE PALO ALTO SQUARE, 4TH FLOOR
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/963,538B
; FILING DATE: 20-OCT-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/843,359
; FILING DATE: 25-FEB-1992
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/408,483
; FILING DATE: 22-AUG-1989
; APPLICATION DATA:
; APPLICATION NUMBER: JP 4-212399
; FILING DATE: 17-JUL-1992
; APPLICATION DATA:
; APPLICATION NUMBER: JP 4-212398
; FILING DATE: 17-JUL-1992
; APPLICATION DATA:
; APPLICATION NUMBER: JP 3-355553
; FILING DATE: 24-DEC-1991
; APPLICATION DATA:
; APPLICATION NUMBER: JP 62-330219
; FILING DATE: 28-DEC-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: NEELEY PH.D., RICHARD L.
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: TEJN-005/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5070
; TELEFAX: 415-857-0663
; TELEX: 380816 COOLEY PA
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 63 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (synthetic)
; US-07-963-538B-31

Alignment Scores:
Pred. No.: 1,11e-05 Length: 63
Score: 124.00 Matches: 21
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 16.27% Indels: 0
DB: 2 Gaps: 0

US-10-613-105-2 (1-132) x US-07-963-538B-31 (1-63)
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QY 74 AppProValAspThrProAsnProThrArgArgLysProGlyLysCysProValThrTyr 93
Db 1 GATCCGTCGACACCCCGAACCGCGTCTGTAAACCGGGTAAATGTCCGGTTACATAT 60

QY 94 Gly 94
Db 61 GGT 63
```

```
RESULT 33
US-08-304-051-12
; Sequence 12, Application US/08304051
; Patent No. 5633227
; GENERAL INFORMATION:
; APPLICANT: Muller, Daniel K.; Brownell, Elise; Delaria, Katherine A.
; TITLE OF INVENTION: Secretory Leukocyte Protease Inhibitor as an
; TITLE OF INVENTION: Inhibitor of Tryptase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Miles Inc.
; STREET: 400 Morgan Lane
; CITY: West Haven
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06516
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1,300 Kb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word Perfect 3.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/304,051
; FILING DATE: 12-Sept-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA: No. 5633227e
; ATTORNEY/AGENT INFORMATION:
; NAME: William F. Gray
; REGISTRATION NUMBER: 31018
; REFERENCE/DOCKET NUMBER: MMH 322
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203) 937-2712
; TELEFAX: (203) 937-2795
; TELEX: 221949 MILES UR
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 89 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; MOLECULE TYPE: - Other nucleic Acid: synthetic
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Primer for Polymerase Chain Reaction used to make mutein
; NAME/KEY: of human SLPI.
US-08-304-051-12
Alignment Scores:
Pred. No.: 1,79e-05 Length: 89
Score: 124.00 Matches: 26
Percent Similarity: 92.86% Conservative: 0
Best Local Similarity: 92.86% Mismatches: 0
Query Match: 16.27% Indels: 2
DB: 1 Gaps: 2
US-10-613-105-2 (1-132) x US-08-304-051-12 (1-89)
QY 25 GlySerGlyLysSerPheLysAlaGlyValCysProProLysLysSerAlaGlnCys--- 43
Db 9 GGCTCTGGAAGTCCCTCAAGCTGGAGTCTGT---CCTAAGAAATCTGCCAGTGCAGA 65
QY 44 LeuArgTyrLysLysProGluCys 51
Db 66 CTTAGATACAAGAACCTGAGTGC 89
RESULT 34
US-08-304-051-13
; Sequence 13, Application US/08304051
; Patent No. 5633227
; GENERAL INFORMATION:
; APPLICANT: Muller, Daniel K.; Brownell, Elise; Delaria, Katherine A.
```

```
; TITLE OF INVENTION: Secretory Leukocyte Protease Inhibitor as an
; TITLE OF INVENTION: Inhibitor of Tryptase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Miles Inc.
; STREET: 400 Morgan Lane
; CITY: West Haven
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06516
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1,300 Kb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word Perfect 3.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/304,051
; FILING DATE: 12-Sept-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA: No. 5633227e
; ATTORNEY/AGENT INFORMATION:
; NAME: William F. Gray
; REGISTRATION NUMBER: 31018
; REFERENCE/DOCKET NUMBER: MMH 322
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203) 937-2712
; TELEFAX: (203) 937-2795
; TELEX: 221949 MILES UR
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 89 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; MOLECULE TYPE: - Other nucleic Acid: synthetic
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Primer for Polymerase Chain Reaction used to make mutein
; NAME/KEY: of human SLPI.
US-08-304-051-13
Alignment Scores:
Pred. No.: 1,79e-05 Length: 89
Score: 124.00 Matches: 26
Percent Similarity: 92.86% Conservative: 0
Best Local Similarity: 92.86% Mismatches: 0
Query Match: 16.27% Indels: 2
DB: 1 Gaps: 2
US-10-613-105-2 (1-132) x US-08-304-051-13 (1-89)
QY 25 GlySerGlyLysSerPheLysAlaGlyValCysProProLysLysSerAlaGlnCys--- 43
Db 9 GGCTCTGGAAGTCCCTCAAGCTGGAGTCTGT---CCTAAGAAATCTGCCAGTGCAGA 65
QY 44 LeuArgTyrLysLysProGluCys 51
Db 66 CTTAGATACAAGAACCTGAGTGC 89
RESULT 35
PCT-US95-11445-12
; Sequence 12, Application PC/TUS9511445
; GENERAL INFORMATION:
; APPLICANT: Muller, Daniel K.; Brownell, Elise; Delaria,
; APPLICANT: Katherine A.
; TITLE OF INVENTION: Secretory Leukocyte Protease
; TITLE OF INVENTION: Inhibitor as an Inhibitor of Tryptase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bayer Corporation
; STREET: 400 Morgan Lane
```

CITY: West Haven
STATE: Connecticut
COUNTRY: USA
ZIP: 06516
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1,300 Kb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word Perfect 3.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11445
FILING DATE: 11 September 1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/304,051
FILING DATE: 12 SEPTEMBER 1994
ATTORNEY/AGENT INFORMATION:
NAME: William F. Gray
REGISTRATION NUMBER: 31018
REFERENCE/DOCKET NUMBER: MWH 322P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 937-2712
TELEFAX: (203) 937-5492
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 89 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
MOLECULE TYPE: - Other nucleic Acid: synthetic
HYPOTHETICAL: No
ANTI-SENSE: No
FEATURE:
NAME/KEY: Primer for Polymerase Chain Reaction used to
NAME/KEY: make mutein of human SLPI.
PCT-US95-11445-12
Alignment Scores:
Pred. No.: 1-79e-05 Length: 89
Score: 124.00 Matches: 26
Percent Similarity: 92.86% Conservative: 0
Best Local Similarity: 92.86% Mismatches: 0
Query Match: 16.27% Indels: 2
DB: 5 Gaps: 2
US-10-613-105-2 (1-132) x PCT-US95-11445-12 (1-89)
Qy 25 GlySerGlyLysSerPhelysAlaGlyValCysProProLysLysSerAlaGlnCys--- 43
Db 9 GGCTCTGGAAGTCCTTCAAGCTGGAGTCTGT---CCTAAGAAATCTGCCAGTGCAGA 65
Qy 44 LeuArgTyrLysLysProGluCys 51
Db 66 CTTAGATACAAGAAACCTGAGTGC 89
RESULT 36
PCT-US95-11445-13
Sequence 13, Application PC/TUS9511445
GENERAL INFORMATION:
APPLICANT: Muller, Daniel K.; Brownell, Elise; Delaria,
APPLICANT: Katherine A.
TITLE OF INVENTION: Secretory Leukocyte Protease
TITLE OF INVENTION: Inhibitor as an Inhibitor of Trypsin
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESS: Bayer Corporation
STREET: 400 Morgan Lane
CITY: West Haven
STATE: Connecticut
COUNTRY: USA
ZIP: 06516
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1,300 Kb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word Perfect 3.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11445
FILING DATE: 11 September 1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/304,051
FILING DATE: 12 SEPTEMBER 1994
ATTORNEY/AGENT INFORMATION:
NAME: William F. Gray
REGISTRATION NUMBER: 31018
REFERENCE/DOCKET NUMBER: MWH 322P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 937-2712
TELEFAX: (203) 937-5492
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 89 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
MOLECULE TYPE: - Other nucleic Acid: synthetic
HYPOTHETICAL: No
ANTI-SENSE: No
FEATURE:
NAME/KEY: Primer for Polymerase Chain Reaction used to
NAME/KEY: make mutein of human SLPI.
PCT-US95-11445-13
Alignment Scores:
Pred. No.: 1-79e-05 Length: 89
Score: 124.00 Matches: 26
Percent Similarity: 92.86% Conservative: 0
Best Local Similarity: 92.86% Mismatches: 0
Query Match: 16.27% Indels: 2
DB: 5 Gaps: 2
US-10-613-105-2 (1-132) x PCT-US95-11445-13 (1-89)
Qy 25 GlySerGlyLysSerPhelysAlaGlyValCysProProLysLysSerAlaGlnCys--- 43
Db 9 GGCTCTGGAAGTCCTTCAAGCTGGAGTCTGT---CCTAAGAAATCTGCCAGTGCAG 65
Qy 44 LeuArgTyrLysLysProGluCys 51
Db 66 CTTAGATACAAGAAACCTGAGTGC 89
RESULT 37
US-09-152-060-34
Sequence 34, Application US/09152060
Patent No. 6448230
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: P2003P1.US
CURRENT APPLICATION NUMBER: US/09/152,060
CURRENT FILING DATE: 1998-09-11
EARLIER APPLICATION NUMBER: PCT/US98/04858
EARLIER FILING DATE: 1998-03-12
EARLIER APPLICATION NUMBER: 60/040,762
EARLIER FILING DATE: 1997-03-14
EARLIER APPLICATION NUMBER: 60/040,710
EARLIER FILING DATE: 1997-03-14
EARLIER APPLICATION NUMBER: 60/050,934
EARLIER FILING DATE: 1997-05-30
EARLIER APPLICATION NUMBER: 60/048,100
EARLIER FILING DATE: 1997-05-30
EARLIER APPLICATION NUMBER: 60/048,357
EARLIER FILING DATE: 1997-05-30

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; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 34
; LENGTH: 753
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-152-060-34

Alignment Scores:
Pred. No.: 0.00171 Length: 753
Score: 117.50 Matches: 47
Percent Similarity: 38.12% Conservative: 14
Best Local Similarity: 29.38% Mismatches: 58
Query Match: 15.42% Indels: 41
DB: 4 Gaps: 10

US-10-613-105-2 (1-132) x US-09-152-060-34 (1-753)

QY 1 MetLysSerSerGlyLeuPheProPheLeuValLeuLeuAlaLeuGlyThrLeuAlaPro 20
DB 31 ATGGGATCTTCTGGACTTTTGAGCCTCTCGGTGCTATTTCCTC-----TTAGCG--- 81

QY 21 TrpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysPro-----Pro 37
DB 82 ---AATGTCAGGACCTGCT-----CTGACTGATTGGTTATTTCAGAGAGATGCCC 132

QY 38 LysLysSerAlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAspTrpGlnCys 57
DB 133 AAAATCAGAGAAGAAATGTGAATCCAAAGAAAGGATGTGTGTACAAAGGACAGACAATGC 192

QY 58 ProGlyLysLysArgCysCysProAspThrCysGlyLysCysLeu----- 73
DB 193 CAGGACAACAAGAAAGTGTGTCTTCAGCTGCGGAAAAAATGTTTAGATCTCAAAACA 252

QY 74 AspProValAspThrProAsnProThr----- 82
DB 253 GATGTATGCAATGCCAAAGAACTGGCCCTGCTGCTATTATTTCTTCATTGTGG 312

QY 83 ---ArgArgLysProGlyLysCysProVal---ThrTyrGlyGlnCys----- 96
DB 313 TATGACAAGAAAGATAATCTTGCTCCATGTTTGTCTATGTGTGCTGCCAGGAAACAAT 372

QY 97 -----LeuMetLeuAsnProProAsnPheCysGlu----- 106
DB 373 AACAACTTCCAAATCCAAAGCAACTGCTGAACACCTGCAAGAAATAAACCGCTTCCCTGA 432

QY 107 MetAspGlyGlnCysLysArgAspLeuLysCysMetGlyMetCysGlyLysSerCys 126
DB 433 TTGGATAAGGATGCATCGGAAGAACTGCCAGAAATGT---GGCTCATGCTCTGAGTACTGT 489

RESULT 38
US-09-270-767-1693
; Sequence 1693, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1693
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-1693

Alignment Scores:
Pred. No.: 0.00304 Length: 472
Score: 112.50 Matches: 25
Percent Similarity: 43.42% Conservative: 8
Best Local Similarity: 32.89% Mismatches: 18
Query Match: 14.76% Indels: 25
DB: 4 Gaps: 3

US-10-613-105-2 (1-132) x US-09-270-767-1693 (1-472)

QY 25 GlySerGlyLys-----SerPheLysAlaGlyValCysPro--- 36
DB 220 GGCTCTGGAAGAAGAAATGCCAGTGGTGGACGTGCGAGGTGAATACTGTCTCTCCA 279

QY 37 -----ProLysLysSerAlaGlnCysLeuArgTyrLysLysPro----- 49
DB 280 GTCCCGCCTGTTTGGCTTAGGAAGCCGGACAGTGTCTTACCTGGTTCACCGGGTCT 339

QY 50 -----GluCysGlnSerAspTrpGlnCysProGly 59
DB 340 GATAACCTGGATGCCAACACCTGTGCTACGAGTGCCTACCGATGCCCATTTGTATGGA 399

QY 60 LysLysArgCysCysProAspThrCysGlyLysCysLeuAspPro 75
DB 400 GCCCGACGCTGTGCTTCCCAATGATGTGGACCCAGTGTGTGATCTCT 447

; ORGANISM: Drosophila melanogaster
US-09-270-767-1693

Alignment Scores:
Pred. No.: 0.00304 Length: 472
Score: 112.50 Matches: 25
Percent Similarity: 43.42% Conservative: 8
Best Local Similarity: 32.89% Mismatches: 18
Query Match: 14.76% Indels: 25
DB: 4 Gaps: 3

US-10-613-105-2 (1-132) x US-09-270-767-1693 (1-472)

QY 25 GlySerGlyLys-----SerPheLysAlaGlyValCysPro--- 36
DB 220 GGCTCTGGAAGAAGAAATGCCAGTGGTGGACGTGCGAGGTGAATACTGTCTCTCCA 279

QY 37 -----ProLysLysSerAlaGlnCysLeuArgTyrLysLysPro----- 49
DB 280 GTCCCGCCTGTTTGGCTTAGGAAGCCGGACAGTGTCTTACCTGGTTCACCGGGTCT 339

QY 50 -----GluCysGlnSerAspTrpGlnCysProGly 59
DB 340 GATAACCTGGATGCCAACACCTGTGCTACGAGTGCCTACCGATGCCCATTTGTATGGA 399

QY 60 LysLysArgCysCysProAspThrCysGlyLysCysLeuAspPro 75
DB 400 GCCCGACGCTGTGCTTCCCAATGATGTGGACCCAGTGTGTGATCTCT 447
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RESULT 40

US-09-152-060-50
; Sequence 50, Application US/09152060
; Patent No. 6448230
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P1.US
; CURRENT APPLICATION NUMBER: US/09/152,060
; CURRENT FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040,762
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040,710
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050,934
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,100
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,357
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
; LENGTH: 783
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-152-060-50

Alignment Scores:
Pred. No.: 0.00614 Length: 783
Score: 112.50 Matches: 47
Percent Similarity: 38.51% Conservative: 15
Best Local Similarity: 29.19% Mismatches: 57
Query Match: 14.76% Indels: 42
DB: 4 Gaps: 10

US-10-613-105-2 (1-132) x US-09-152-060-50 (1-783)

Qy 1 MetLysSerSerGlyLeuPheProPheLeuValLeuLeuAlaLeuGlyThrLeuAlaPro 20
Db 31 ATGGMTCTTCTGGACTTTTGGAGCTCTCTGGTCTATTTCGTCCTC-----TTAGCG--- 81
Qy 21 TrpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysPro-----Pro 37
Db 82 ---AATGTCAGGAGCCTGCT-----CTGACTGATTGGTTATTTCCTCCAGGAGATGTC 132
Qy 38 LysLysSerAlaGlnCysLeuAlaGlyTyrLysProGluCysGlnSerAspTrpGlnCys 57
Db 133 AAATCAGAGAAGATGTGAATCCAGAAGGAGTGTGTACAAAGGACAGACATGC 192
Qy 58 ProGlyLysLysArgCysCysProAspThrCysGlyLysCysLeu----- 73
Db 193 CAGGACAAACAAGAGTGTGTCTTCAGCTCGGAAAAAATGTTTAGATCTCAACAA 252
Qy 74 AspProValAspThrProAsnProThr----- 82
Db 253 GATGTATGCGAAATGCCAAAGAACTGGCCCTGCTGCTTATTTTCTTCATTGTTGG 312
Qy 83 ---ArgArgLysProGlyLysCysProVal---ThrTyrGlyGlnCys----- 96
Db 313 TATGACAAAGAAGATAATACTTGTCTTCCATGTTTGTCTATGTTGGTCCAGGGGAACAA 372
Qy 97 -----LeuMetLeuAsnProPro-AsnPheCysGlu----- 106

Db 373 TAACAACCTTCCAAATCCAAAGCCAACTGCCTTGAACACCTGCAGAAATAAAGCTTTCCTG 432
Qy 107 -MetAspGlyGlnCysLysArgAspLeuLysCysCysMetGlyMetCysGlyLysSerCy 126
Db 433 ATTGGATAAGGATGCACTGGAAGAACTGCCAGAATGT---GGCTCATGCTCTGAGTACTG 489
Qy 126 s 126
Db 490 T 490
RESULT 41
US-09-383-586-29
; Sequence 29, Application US/09383586
; Patent No. 6242419
; GENERAL INFORMATION:
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Abernethy, Nevin
; APPLICANT: Onrust, Rene
; APPLICANT: Kumble, Anand
; APPLICANT: Murison, Greg
; TITLE OF INVENTION: Compounds isolated from stromal cells
; FILE REFERENCE: 11000.1037c1
; CURRENT APPLICATION NUMBER: US/09/383,586
; CURRENT FILING DATE: 1999-08-26
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 437
; TYPE: DNA
; ORGANISM: Mouse
US-09-383-586-29

Alignment Scores:
Pred. No.: 0.00568 Length: 437
Score: 109.50 Matches: 39
Percent Similarity: 39.71% Conservative: 15
Best Local Similarity: 28.68% Mismatches: 61
Query Match: 14.37% Indels: 21
DB: 3 Gaps: 7

US-10-613-105-2 (1-132) x US-09-383-586-29 (1-437)

Qy 9 PheLeuVal---LeuLeuAlaLeuGlyThrLeuAlaProTrpAlaValGluGlySerGly 27
Db 11 TTTCTGGTGGCTTTGATCAGCTGTGGGATGCAACACTACCTATGATGTTCTTGGCCCAA 70
Qy 28 LysSerPheLysAlaGlyValCysProProLysLysSerAlaGlnCysLeuAlaGlyTyrLys 47
Db 71 GAATTTGAAAAACCTGGAGCTTGT---CCCAAGCCTTCCACGAAAGTGTGGAAATTTGT 127
Qy 48 LysProGluCysGlnSerAspTrpGlnCysProGlyLysLysArgCysCysProAspThr 67
Db 128 GTTGATCAATGCTCAGAGATGATGCTGCTCCCTGGCAACATGAAGTCTGTAGCAATAGC 187
Qy 68 CysGlyLysCysLeuAspProVal-----AspThr 78
Db 188 TGTGGTCATGCTGCAAACTCTCTGCTTTTAATGTTGACAGCCATGTTGGAAGATGGA 247
Qy 79 ProAsnProThrArgArgLysProGlyLysCysProValThrTyr-----Gly 94
Db 248 TTCAATCTTCATAAATCATGAATGATGGCCAGCCCAAGAGATTTCTTCTGAATTCACAGA 307
Qy 95 GlnCysLeuMetLeuAsnPro---ProAsnPheCysGluMetAspGlyGlnCysLysArg 113
Db 308 GCCTGTGCTTGGTACTTCTCTGCTAGCAATGCTTCTGGAC-----AAGGAA 358
Qy 114 AspLeuLysCysCysMetGlyMetCysGlyLysSerCysValSerPro 129
Db 359 GATCTATATTGT-----GGTGCAATGCCCTAATATGTTCTGTGTCCA 400

RESULT 42

US-09-823-038A-29
; Sequence 29, Application US/09823038A
; Patent No. 6797271
; GENERAL INFORMATION:
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Abernethy, Nevin
; APPLICANT: Onrust, Rene
; APPLICANT: Kumbie, Anand
; APPLICANT: Murison, Greg
; TITLE OF INVENTION: Compositions Isolated From Stromal Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1037c3
; CURRENT APPLICATION NUMBER: US/09/823.038A
; CURRENT FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 437
; TYPE: DNA
; ORGANISM: Mouse
US-09-823-038A-29

Alignment Scores:
Pred. No.: 0.00568 Length: 437
Score: 109.50 Matches: 39
Percent Similarity: 39.71% Conservative: 15
Best Local Similarity: 28.68% Mismatches: 61
Query Match: 14.37% Indels: 21
DB: 4 Gaps: 7

US-10-613-105-2 (1-132) x US-09-823-038A-29 (1-437)

Qy 9 PheLeuVal---LeuLeuAlaLeuGlyThrLeuAlaProTrpAlaValGluGlySerGly 27
Db 11 TTCTGTGGCTTTGATGCTGGGATGAACTACTATGATGATGCTTGGCCCAA 70
Qy 28 LysSerPheLysAlaGlyValCysProPheLysSerAlaGlnCysLeuArgTyrLys 47
Db 71 GAATTTGAAAACCTGGAGCTTGT---CCCAAGCTTCACAGAAAGTGTGGAAATTTGT 127
Qy 48 LysProGluCysGlnSerAspTTPGlnCysProGlyLysArgCysCysProAspThr 67
Db 128 GTTGATCAATGCTCAGAGATGGATCTGCTGGCCGCAACATGAAGTCTGTAGCAATAGC 187
Qy 68 CysGlyIleLysCysLeuAspProVal-----AspThr 78
Db 188 TGTGGTCATGCTGCAAAACCTCTGTCTTTTAAATGTTGACAGCCATGTGGAAGATGGA 247
Qy 79 ProAsnProThrArgArgLysProGlyLysCysProValThrTyr-----Gly 94
Db 248 TTCAATCTTCATAAACATGAATGATGCGCCAGCCCAAGATTTCTTCTGAATTCACAGA 307
Qy 95 GlnCysLeuMetLeuAsnPro---ProAsnPheCysGluMetAspGlyGlnCysLysArg 113
Db 308 GCCTGTGCTGGCTACTCTCTAGCCCTAGATTCATTCCTTGGAC-----AAGGAA 358
Qy 114 AspLeuLysCysCysMetGlyMetCysGlyLysSerCysValSerPro 129
Db 359 GATCTATATTGT-----GGTGACAATGCCCTAATATGATGCTGTGTCCA 400

RESULT 43

US-07-978-895-3
; Sequence 3, Application US/07978895
; Patent No. 5480968
; GENERAL INFORMATION:
; APPLICANT: Kraus, Matthias H.
; APPLICANT: Aaronson, Stuart A.
; TITLE OF INVENTION: AN ISOLATED POLYPEPTIDE RELATED TO THE
; TITLE OF INVENTION: EPIDERMAL GROWTH FACTOR RECEPTOR, ANTIGEN THEREOF, AND
; TITLE OF INVENTION: BIOASSAYS AND METHODS RELATED THEREOF
; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Suite 400
; STREET: 133 Carnegie Way, N.W.
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: U.S.A.
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/978,895
; FILING DATE: 19921110
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/444,406
; FILING DATE: 01-DEC-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Periyman, David G.
; REGISTRATION NUMBER: 33,438
; REFERENCE/DOCKET NUMBER: 1414-028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 688-0770
; TELEFAX: (404) 688-9880
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4905 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 100..4125
; US-07-978-895-3

Alignment Scores:
Pred. No.: 0.186 Length: 4905
Score: 109.00 Matches: 41
Percent Similarity: 32.32% Conservative: 12
Best Local Similarity: 25.00% Mismatches: 43
Query Match: 14.30% Indels: 68
DB: 1 Gaps: 9

US-10-613-105-2 (1-132) x US-07-978-895-3 (1-4905)
Qy 23 ValGluGlySerGlyLysSerPheLysAlaGlyValCysProPro----- 37
Db 625 GTGAGGACAATGGCAGAAC-----TGTCCTCCCTGTCATGAGGTTTGC 669
Qy 38 -----LysLysSerAlaGlnCysLeuArgTyrLysLys----- 48
Db 670 AAGGGCGATGCTGGGGTCTCTGGATCAGAAGACTGCGACATTTGACCAAGACCATCTGT 729
Qy 49 ---ProGluCysGlnSerAspTTPGlnCysProGlyLysLysArgCysCysProAspThr 67
Db 730 GCTCTTCAGTGTAATGGTCACTGCTCTTGGGCCCCAACCCCAACCGATGCTGCCATGATGAG 789
Qy 68 CysGlyIleLysCysLeuAspProValAspThr----- 78
Db 790 TGTGCCGGGGCTGCTCAGGCCCTCAGGACACAGACTGCTTTGCTGCCGCACTTCAAT 849
Qy 78 ----- 78
Db 850 GACAGTGGAGCCTGTGTACCTCGCTGTCCACAGCCTCTTGTCTACAACAGCTAATCTTC 909
Qy 79 -----ProAsnPro---ThrArgLysProGly-----LysCys 89
Db 910 CAGCTGGAAACCAATCCCAACCAAGTATCAGTATGGAGGAGTTGTGTAGCCAGCTGT 969
Qy 90 Pro-----ValThrTyrGlyGlnCysLeuMetLeuAsnProProAsnPheCys 105

Db 970 CCCATAACTTTGGTGGATCAACATCTGTGTCTCAGGGCCTGTCTCTCTGCAAGATG 1029
Qy 106 GluMetAspGlyGlnCysLysAlaGlyLeuLysCysCysMet-----GlyMetCys 122
Db 1030 GAAGTAGAT-----AAAAATGGGCTCAAGATGTGTGAGCCTTGTGGGGGACTATGT 1080

Qy 123 GlyLysSerCys 126

Db 1081 CCCAAGCCTGT 1092

RESULT 44

US-08-473-119-3
; Sequence 3, Application US/08473119
; Patent No. 5820859
; GENERAL INFORMATION:
; APPLICANT: Kraus, Matthias H.
; APPLICANT: Aaronson, Stuart A.
; TITLE OF INVENTION: AN ISOLATED POLYPEPTIDE RELATED TO THE
; TITLE OF INVENTION: EPIDERMAL GROWTH FACTOR RECEPTOR, ANTIGEN THEREO, AND
; TITLE OF INVENTION: BIOASSAYS AND METHODS RELATED THEREO
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Suite 400
; STREET: 133 Carnegie Way, N.W.
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: U.S.A.
; ZIP: 30303

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/473,119
; FILING DATE: 07-JUN-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/978,895

FILING DATE: 10-NOV-1992

APPLICATION NUMBER: US 07/444,406

FILING DATE: 01-DEC-1989

ATTORNEY/AGENT INFORMATION:

NAME: Perryman, David G.

REGISTRATION NUMBER: 33,438

REFERENCE/DOCKET NUMBER: 1414-028

TELECOMMUNICATION INFORMATION:

TELEPHONE: (404) 688-9880

TELEFAX: (404) 688-9880

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 4905 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 100..4125

US-08-473-119-3

Alignment Scores:

Pred. No.:	0.186	Length:	4905
Score:	109.00	Matches:	41
Percent Similarity:	32.32%	Conservative:	12
Best Local Similarity:	25.00%	Mismatches:	43
Query Match:	14.30%	Indels:	68
DB:	1	Gaps:	9

US-10-613-105-2 (1-132) x US-08-473-119-3 (1-4905)

Qy 23 ValGluGlySerGlyLysSerPheLysAlaGlyValCysPro----- 37

Db 625 GTGAAGGACAATGGCAGAAGC-----TGTCCTCCCTGTCATGAGTTTGC 669

Qy 38 -----LysLysSerAlaGlnCysLeuArgTyrLysLys----- 48

Db 670 AAGGGCGGATGCTGGGGTCTCTGGATCAGAAGATGCGAGACATTGACCAAGACCATCTGT 729

Qy 49 ---ProGluCysGlnSerAspTrpGlnCysProGlyLysLysArgCysCysProAspThr 67

Db 730 GCTCCTCAGTGTAAATGCTCACTGCTTTGGGCCCAACCCCAACCAAGCTGCTCCATGATGAG 789

Qy 68 CysGlyLysLysCysLeuAspProValAspThr----- 78

Db 790 TGTGCCCGGGGCTGCTCAGGCCCTCAGGACACAGACTGCTTTGCCCTGCCGACATTCAAT 849

Qy 78 ----- 78

Db 850 GACAGTGGAGCCTGTGTACCTCCTGCTCCACAGCCTCTTGTCTACAACAAGCTAACTTTC 909

Qy 79 -----ProAsnPro---ThrArgAlaGlyProGly-----LysCys 89

Db 910 CAGCTGGAACCCCAATCCCCACACCAAGTATCACTATGAGGAGTGTGTGAGCCAGCTGT 969

Qy 90 Pro-----ValThrTyrGlyGlnCysLeuMetLeuAsnProProAsnPheCys 105

Db 970 CCCATAAATTTGTGTGGTGGATCAACATCCTGTGTGTCAGGGCCTGTCTCTCTGCAAGATG 1029

Qy 106 GluMetAspGlyGlnCysLysAlaGlyLeuLysCysCysMet-----GlyMetCys 122

Db 1030 GAAGTAGAT-----AAAAATGGGCTCAAGATGTGTGAGCCTTGTGGGGGACTATGT 1080

Qy 123 GlyLysSerCys 126

Db 1081 CCCAAGCCTGT 1092

RESULT 45

US-08-475-352-3

; Sequence 3, Application US/08475352

; Patent No. 5916755

; GENERAL INFORMATION:

; APPLICANT: Kraus, Matthias H.

; APPLICANT: Aaronson, Stuart A.

; TITLE OF INVENTION: AN ISOLATED POLYPEPTIDE RELATED TO THE

; TITLE OF INVENTION: EPIDERMAL GROWTH FACTOR RECEPTOR, ANTIGEN THEREO, AND

; TITLE OF INVENTION: BIOASSAYS AND METHODS RELATED THEREO

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Suite 400

; STREET: 133 Carnegie Way, N.W.

; CITY: Atlanta

; STATE: Georgia

; COUNTRY: U.S.A.

; ZIP: 30303

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/475,352

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/978,895

; FILING DATE:

; APPLICATION NUMBER: US 07/444,406

; FILING DATE: 01-DEC-1989

; ATTORNEY/AGENT INFORMATION:

; NAME: Perryman, David G.

; REGISTRATION NUMBER: 33,438

; REFERENCE/DOCKET NUMBER: 1414-028

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (404) 688-0770

TELEFAX: (404) 688-9880
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4905 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 100..4125
US-08-475-352-3

Alignment Scores:

Pred. No.:	0.186	Length:	4905
Score:	109.00	Matches:	41
Percent Similarity:	32.32%	Conservative:	12
Best Local Similarity:	25.00%	Mismatches:	43
Query Match:	14.30%	Indels:	68
DB:	2	Gaps:	9

US-10-613-105-2 (1-132) x US-08-475-352-3 (1-4905)

QY	23	ValGluGlySerGlyLysSerPheLysAlaGlyValCysProPro-----	37
DB	625	GTGAGGACAAATGCCAGAAC-----TGTCCTCCCTGTCATGAGTTTGC	669
QY	38	-----LysLysSerAlaGlnCysLeuArgTyrLysLys-----	48
DB	670	AAGGGGCGATGCTGGGTCTGGATCAGAGACTGCCAGACATTGACCAAGACCATCTGT	729
QY	49	---ProGluCysGlnSerAspTTPGlnCysProGlyLysArgCysProAspThr	67
DB	730	GCTCCTCAGTGAATGTCTACTGCTTTGGGCCCAACCCCAACAGTGTCTGCCATGATGAG	789
QY	68	CysGlyIleLysCysLeuAspProValAspThr-----	78
DB	790	TGTGCCGGGGCTGCTCAGGCCCTCAGGACACAGACTGCTTTGCCTGCCGGCATTCAAT	849
QY	78	-----	78
DB	850	GACAGTGGAGCCTGTGTACCTGCTGTCCACAGCCTTGTCTACACAAAGCTAACTTTC	909
QY	79	-----ProAsnPro---ThrArgArgLysProGly-----LysCys	89
DB	910	CAGCTGGAACCCCAATCCCAACAGATATCAGTATGGAGGAGTTTGTGTAGCCAGCTGT	969
QY	90	Pro-----ValThrTyrGlnCysLeuMetLeuAsnProProAsnPheCys	105
DB	970	CCCATAAATTTGTGTGGATCAACATCCTGTGTACAGGCTGTCTCTCTGACAAGATG	1029
QY	106	GluMetAspGlyGlnCysLysArgAspLeuLysCysMet-----GlyMetCys	122
DB	1030	GAAGTAGAT-----AAAAATGGGCTCAAGATGTGTGAGCCTTGTGGGGGACTATGT	1080
QY	123	GlyLysSerCys	126
DB	1081	CCCAAGACCTGT	1092

Search completed: October 24, 2004, 05:53:46
Job time : 94 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 24, 2004, 02:50:16 ; Search time 432 Seconds
(without alignments)
1603.990 Million cell updates/sec

Title: US-10-613-105-2

Perfect score: 762

Sequence: 1 MKSSGLFPFLVLALGTLP.....RDLKCCMGCKSCVSPVKA 132

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DRV=xlh
-Q=/cgn2_1/USPTO_spool_h/US10613105/runat_22102004_170440_18681/app_query.fasta_1.327
-DB=N_Geneseq_23Sep04 -Qfmt=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi
-LIST=100 -DOALIGN=200 -THR SCORE=pcp -THR MAX=100 -THR MIN=0 -ALIGN=45
-MODE=LOCAL -OUTPMT=ptto -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10613105 @CGN 1.1 470 @runat_22102004_170440_18681 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEW_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: N_Geneseq_23Sep04:*
- 2: Geneseqn1980s:*
- 3: Geneseqn1990s:*
- 4: Geneseqn2000s:*
- 5: Geneseqn2001as:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	762	100.0	399	5	ABA83108
2	762	100.0	422	10	AD95609
3	762	100.0	551	10	AD79666
4	762	100.0	565	1	AAN70930
5	762	100.0	565	4	AAF32043
6	762	100.0	594	6	ABS76518

7	762	100.0	594	6	ABL67548	Thyroid c
8	762	100.0	594	6	ABL66679	Lung canc
9	762	100.0	594	6	AA517499	Human CDN
10	762	100.0	594	6	ABT11084	Human bre
11	762	100.0	594	8	AB234724	Coding se
12	762	100.0	594	8	ACC50295	Breast ca
13	762	100.0	594	10	ADB75550	Prostate
14	762	100.0	594	10	ADB95611	Human NOV
15	762	100.0	594	10	ADF81611	Leukaemia
16	762	100.0	594	10	ACA56673	Human sig
17	762	100.0	594	10	ADK61171	Ovarian c
18	762	100.0	594	11	ADP65640	Human mRN
19	762	100.0	594	12	AD156469	Human pol
20	762	100.0	598	8	ACG50296	Breast ca
21	762	100.0	598	10	ADB80589	Ovarian c
22	762	100.0	598	11	ADP65076	Human sec
23	762	100.0	598	12	ADL26771	Human SLP
24	762	100.0	598	12	ADN03925	Antipeori
25	762	100.0	599	2	AAZ77546	Human ova
26	762	100.0	636	4	AAH57451	Human lun
27	762	100.0	1084	5	ADL62375	Human ova
28	756	99.1	594	12	ADL57146	Human NOV
29	755	99.1	594	12	ADL57144	Human NOV
30	754	99.0	594	12	ADL57140	Human NOV
31	750	98.4	594	12	ADL57142	Human NOV
32	750	98.4	594	12	ADL57148	Human NOV
33	745	97.8	567	10	ADK11941	Breast ca
34	723	94.9	594	12	ADL57150	Human NOV
35	720	94.6	605	9	AAAL60894	Human sec
36	703	92.3	528	10	ADK61172	Ovarian c
37	645	84.6	460	2	AAK16271	DNA seque
38	645	84.6	460	3	AAK97622	DNA seque
39	645	84.6	460	4	AAI67582	DNA seque
40	638	83.8	1525	6	ABK88025	DNA seque
41	635	83.3	321	6	ABK88016	Human NOV
42	635	83.3	321	10	AD95613	Human NOV
43	635	83.3	324	1	AAN60463	Serine pr
44	635	83.3	324	1	AAN60464	Synthetic
45	635	83.3	324	2	AAK16236	Serine pr
46	635	83.3	324	2	AAK16169	Serine pr
47	635	83.3	324	3	AAK97579	DNA seque
48	635	83.3	324	3	AAK97527	DNA seque
49	635	83.3	324	3	AAK97528	Secretory
50	635	83.3	324	4	AAI67488	Secretory
51	635	83.3	324	4	AAI67489	Recombina
52	635	83.3	324	4	AAK97624	DNA seque
53	635	83.3	324	4	AAI67583	DNA seque
54	635	83.3	1525	6	ABK88022	DNA seque
55	631	82.8	420	2	AAK16272	DNA seque
56	624	81.9	324	12	ADL57138	Human NOV
57	597	78.3	314	4	AAH57243	Human lun
58	597	78.3	314	10	ADK11942	Breast ca
59	596	78.2	321	3	AAK97529	DNA seque
60	557.5	73.2	1072	12	ADK70406	Respirato
61	547	71.8	2274	1	AAN60465	Synthetic
62	547	71.8	2274	3	AAK97530	Human gen
63	547	71.8	2274	4	AAI67491	Recombina
64	545	71.5	498	1	AAN70929	Sequence
65	539	70.7	920	1	AAN60468	ompA-ecr
66	535	70.2	872	1	AAN60469	ompA-ec-m
67	463.5	60.8	396	6	ABQ73677	Murine SL
68	463.5	60.8	396	6	ABQ73674	Murine SL
69	463.5	60.8	409	8	ABZ34649	Coding se
70	463.5	60.8	691	2	AAK18514	Mouse IMC
71	463.5	60.8	1114	2	AAK18515	Mouse IMC
72	458	60.1	325	10	ACA56426	Human sig
73	458	60.1	325	12	ADI56222	Human pol
74	378	49.6	684	2	AAK18516	Mouse IMC
75	348	45.7	194	1	AAN90354	Sequence
76	346	45.4	180	1	AAK97526	DNA seque
77	346	45.4	183	2	AAK16273	Secretory
78	346	45.4	183	2	AAI67584	Secretory
79	339	44.5	180	2	AAQ45442	CLPI. 3/2

80 339 44.5 180 3 AA288483 Truncated
 81 339 44.5 805 9 ACH04226 Human cDN
 82 285 37.4 4090 6 AAD45347 Mouse ant
 83 283.5 37.2 313 5 ADI70084 Human ova
 84 283.5 37.2 313 5 ADI76414 Human ova
 85 272 35.7 135 3 AAC97619 DNA inser
 86 272 35.7 135 3 AAC97576 Insert B
 87 272 35.7 135 4 AAI67538 Serine pr
 88 264 34.6 411 6 ABL67811 Ovary can
 89 264 34.6 411 6 ABL66677 Lung canc
 90 264 34.6 411 6 ABL67461 Thyroid c
 91 264 34.6 411 6 ABK64114 Human ben
 92 257.5 33.8 248 12 ADL85843 DNA up-re
 93 257.5 33.8 248 12 ADL85844 DNA up-re
 94 243 31.9 188 5 ADL1650 Human ova
 95 238 31.2 120 3 AAC97577 Insert C
 96 238 31.2 120 3 AAC97620 DNA inser
 97 238 31.2 120 4 AAI67539 Serine pr
 98 224 29.4 292 3 AAA70066 Human ova
 99 224 29.4 292 6 ABA72960 Ovarian c
 100 224 29.4 292 9 ADA08530 Human ova

ALIGNMENTS

RESULT 1
 ABA83108
 ID ABA83108 standard; DNA; 399 BP.
 XX AC ABA83108;
 XX DT 08-FEB-2002 (first entry)
 XX DE Secretory leukocyte protease inhibitor ovarian tumour marker gene, #53.
 XX KW Ovarian tumour marker gene; human; overexpression; upregulation;
 KW epithelial tumour; cancer; diagnosis; prognosis; disease monitoring;
 KW identification; serous cystadenoma; borderline serous tumour;
 KW serous cystadenocarcinoma; mucinous cystadenocarcinoma;
 KW mucinous cystadenoma; borderline mucinous tumour; endometrioid carcinoma;
 KW undifferentiated carcinoma; clear cell adenocarcinoma; cystadenofibroma;
 KW adenofibroma; Brenner tumour; serial analysis of gene expression; SAGE;
 KW immune response pathway; cell proliferation regulation; protein folding;
 KW membrane localised; secreted; therapeutic target; cytostatic;
 KW gene therapy; vaccine; ds.
 XX OS Homo sapiens.
 XX PN WO200175177-A2.
 XX PD 11-OCT-2001.
 XX PF 03-APR-2001; 2001WO-0194336P.
 XX PR 03-APR-2000; 2000US-0194336P.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Morin PJ, Sherman-Baust CA, Pizer ES, Hough CD;
 XX WPI; 2001-626450/72.
 XX DR P-PSDB; ABB50282.
 XX PT Detecting and identifying ovarian tumor, identifying increased risk for
 PT developing ovarian cancer, and determining effectiveness of ovarian
 PT cancer treatment, by measuring expression level of ovarian tumor marker
 PT gene.
 XX PS Claim 23; Page 98; 140pp; English.
 XX CC The invention relates to methods for diagnosing and prognosing ovarian
 CC tumours in an individual via the detection and measurement of the
 CC expression of ovarian tumour marker genes (ABA83081-ABA83122, ABA83180,

CC ABA83182 and ABA83184) or segments thereof (ABA83123-ABA83169, ABA83179,
 CC ABA83181 and ABA83183). The methods of the invention are useful for
 CC detecting an ovarian tumour in a patient, for identifying an individual
 CC at increased risk for developing ovarian cancer, in prognostic tests for
 CC assessing the relative severity of ovarian cancer, in tests for
 CC monitoring a patient in remission from ovarian cancer and in tests for
 CC monitoring disease status in a patient being treated for ovarian cancer.
 CC The methods can additionally be used to identify a particular tumour as
 CC being an ovarian tumour (i.e., an epithelial ovarian tumour selected from
 CC serous cystadenoma, borderline serous tumour, serous cystadenocarcinoma,
 CC mucinous cystadenoma, borderline mucinous tumour, mucinous
 CC cystadenocarcinoma, endometrioid carcinoma, adenofibroma and Brenner
 CC clear cell adenocarcinoma, cystadenofibroma, adenofibroma and Brenner
 CC tumour. The ovarian tumour marker genes of the invention were identified
 CC using SAGE (serial analysis of gene expression) and were found to be
 CC overexpressed in a broad variety of ovarian epithelial tumour cells
 CC relative to normal ovarian epithelial cells. The marker genes are
 CC implicated in immune response pathways, in the regulation of cell
 CC proliferation and in protein folding, and many of these are membrane-
 CC localised or secreted. In addition to their use as diagnostic and
 CC prognostic markers, the ovarian tumour marker genes or their encoded
 CC proteins may be used as therapeutic targets for the treatment and
 CC prevention of ovarian cancer. Sequences ABA83081-ABA83122, ABA83180,
 CC ABA83182 and ABA83184 represent the ovarian tumour marker genes of the
 CC invention
 XX SQ Sequence 399 BP; 91 A; 100 C; 111 G; 97 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1.3e-58 Length: 399
 Score: 762.00 Matches: 132
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 5
 US-10-613-105-2 (1-132) x ABA83108 (1-399)
 QY 1 MetLysSerSerGlyLeuPheProPheLeuValLeuLeuAlaLeuGlyThrLeuAlaPro 20
 DB 1 ATGAAGTCCAGCGGCTCTTCCCTTCTGGTGTCTCTTGGCTGGAACTCTGGCACCT 60
 QY 21 TtpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProLysLysSer 40
 DB 61 TGGGCTGTGGAGGCTCTGGAAGTCTTCAAGCTGGAGTCTGTCTCTCTAGAAATCT 120
 QY 41 AlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAspTrpGlnCysProGlyLys 60
 DB 121 GCCACGTGCTTAGATACAAAGAAACCTGAGTGCAGAGTACTGGCAGTGTCCAGGGAAG 180
 QY 61 LysArgCysCysProAspThrCysGlyLysCysLeuAspProValAspThrProAsn 80
 DB 181 AAGAGATGTTGCTCTGACACATCTGTGCATCAAAATGCTGGATCTCTGTGACACCCCAAC 240
 QY 81 ProThrArgArgLysProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAsn 100
 DB 241 CCACCAAGGAGGAGGCTGGGAGTGCACCATGCTATGGCCCAATGTTGATGCTTAAC 300
 QY 101 ProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGly 120
 DB 301 CCCCCCAATTTCTGTGAGATGGATGCCAGTGCAGCGTGACTTGAAGTGTTCATGGGCG 360
 QY 121 MetCysGlyLysSerCysValSerProValLysAla 132
 DB 361 ATGTGTGGGAAATCTCGCGCTTTCCCTGCTGAAAGCT 396
 RESULT 2
 ADE95609
 ID ADE95609 standard; cDNA; 422 BP.
 XX AC ADE95609;
 XX DT 12-FEB-2004 (first entry)

XX (DEKB-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAFE-) HAFERLACH T.
PA (SCHO/) SCHOCH C.
PA (KERN/) KERN W.
XX
PI Haferlach T, Schoch C, Kern W, Kohlmann A, Schnittger S, Dugas M;
PI Bils R, Brors B, Mergenthaler S;
XX WPI; 2003-505037/47.
XX
XX Determining the subtype of leukemia cells and whether a patient sample
XX contains leukemia cells or other cells, useful for treating leukemia,
XX PT comprises determining the expression profile of a group of markers in a
XX PT patient sample.
XX
XX Disclosure; SEQ ID NO 222; 2938pp; English.
XX
XX The present invention relates to a method (M1) for determining the
XX CC subtype of leukaemia cells and whether a patient sample contains
XX CC leukaemia cells. The method comprises determining the expression profile
XX CC of a group of markers in a patient sample. The method is useful for
XX CC determining the presence of leukaemia cells, its types or subtypes, and
XX CC for the preparation of a medicament for treating leukaemia.
XX
XX Sequence 551 BP; 117 A; 146 C; 150 G; 138 T; 0 U; 0 Other;
XX

Alignment Scores:
Pred. No.: 1.91e-58 Length: 551
Score: 762.00 Matches: 132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-613-105-2 (1-132) x ADF79666 (1-551)
QY 1 MetLysSerSerGlyLeuPheProPheLeuValLeuLeuAlaLeuGlyThrLeuAlaPro 20
DB 14 ATGAAGTCACAGCGGCTCTTCCCTTCTGGTGTCTTCCCTTCCCTAGGAACTCTGGCACCT 73
QY 21 TrpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProProLysLysSer 40
DB 74 TGGGCTGTGGAGGCTCTGGAAGTCTTCAAGCTGGAGTCTGTCTCTTAAGAAATCT 133
QY 41 AlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAspTrpGlnCysProGlyLys 60
DB 134 GCCCAGTGCCTTAGATACAAAGAACCTGAGTGGCAGAGTGACTGGCAGTGCTCCAGGGAAG 193
QY 61 LysArgCysCysProAspThrCysGlyLysLysCysLeuAspProValAspThrProAsn 80
DB 194 AAGAGATGTTGTCTGACACTTGTGGCATCAAAATGCTGGATCTGTGTGACACCCCAAC 253
QY 81 ProThrArgArgLysProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAsn 100
DB 254 CCAACAAGGAGGAGGAGCTGGGAGTGGCCAGTACCTATGAGTGGCCATGTTTGTATGCTTAAC 313
QY 101 ProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysMetGly 120
DB 314 CCCCCCAATTTCTGTGAGATGGATGGCCAGTGGCAAGGCTGACTTGAAGTGTTCATGGGC 373
QY 121 MetCysGlyLysSerCysValSerProValLysAla 132
DB 374 ATGTGTGGGAAATCTGCGCTTTCCCTGTGAAAGCT 409

RESULT 4
AA70930
ID AA70930 standard; cDNA; 565 BP.
XX
AC AA70930;
XX
DT 25-MAR-2003 (revised)

DT 21-MAY-1991 (first entry)
XX
DE Sequence encoding protein with the biological activity of HUS1 (human
DE seminal plasma inhibitor) type I inhibitors encoded on PRH 34.
XX
KW Bronchitis therapy; cervix inflammation; hyperfibrinolysis; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 59..457
FT /*tag= a
XX
XX DE3600571-A.
XX PN
XX 06-AUG-1987.
XX PD
XX 10-JAN-1986; 86DE-03600571.
XX PF
XX 10-JAN-1986; 86DE-03600571.
XX PR
XX (CHEF) GRUENTHAL GMBH.
XX PA
XX Heinzl R, Appelhans H, Gassen HG, Machleidt W;
XX PI WPI; 1987-222038/32.
XX DR P-PSDB; AAP70584.
XX

New protein with human seminal plasma inhibitor activity - and new DNA
coding sequences, vectors and transformed organisms, useful e.g. for
treating bronchitis or inflammation.
XX
XX Claim 5; Fig 5; 28pp; German.
XX PS
XX HUS1-type I inhibitors are useful for treating chronic bronchitis,
XX CC chronic cervical inflammation; inflammation associated with excessive
XX CC mucus prodn.; post-operative bleeding caused by hyperfibrinolysis, and
XX CC shock. They are esp. suitable for administration as spray or inhalation.
XX CC The expression control sequence on the DNA fragment in AAN70928 is bound
XX CC to the 5' end of HUS1 cDNA in an expression vector. (Updated on 25-MAR-
XX CC 2003 to correct PA field.)
XX
SQ Sequence 565 BP; 106 A; 162 C; 171 G; 126 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.96e-58 Length: 565
Score: 762.00 Matches: 132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-10-613-105-2 (1-132) x AAN70930 (1-565)
QY 1 MetLysSerSerGlyLeuPheProPheLeuValLeuLeuAlaLeuGlyThrLeuAlaPro 20
DB 59 ATGAAGTCACAGCGGCTCTTCCCTTCTGGTGTCTTCCCTTCCCTAGGAACTCTGGCACCT 118
QY 21 TrpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProProLysLysSer 40
DB 119 TGGGCTGTGGAGGCTCTGGAAGTCTTCAAGCTGGAGTCTGTCTCTTAAGAAATCT 178
QY 41 AlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAspTrpGlnCysProGlyLys 60
DB 179 GCCCAGTGCCTTAGATACAAAGAACCTGAGTGGCAGAGTGACTGGCAGTGCTCCAGGGAAG 238
QY 61 LysArgCysCysProAspThrCysGlyLysLysCysLeuAspProValAspThrProAsn 80
DB 239 AAGAGATGTTGTCTGACACTTGTGGCATCAAAATGCTGGATCTGTGTGACACCCCAAC 298
QY 81 ProThrArgArgLysProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAsn 100
DB 299 CCAACAAGGAGGAGGCTGGGAGTGGCCAGTACCTATGAGTGGCCAAATGTTTGTATGCTTAAC 358

CC The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms' tumour

SQ Sequence 594 BP; 132 A; 156 C; 155 G; 151 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 2,08e-58 Length: 594
 Score: 762.00 Matches: 132
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-613-105-2 (1-132) x ABL67548 (1-594)

QY 1 MetLysSerGlyLeuPheProPheLeuValLeuAlaLeuGlyThrLeuAlaPro 20
 DB 19 ATGAAGTCCAGCGGCTCTTCCCTTCCTGCTGCTGCCCTGGGAACCTGGCACCT 78
 QY 21 TrpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProLysLysSer 40
 DB 79 TGGCTGTGGAAGCTCTGGAAGTCTTCAAAGCTGGAGTGTCTCTCTAAGAAATCT 138
 QY 41 AlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAspTyrGlnCysProGlyLys 60
 DB 139 GCCAGTGCCTTAGATACAGAAACCTGAGTGCAGAGTACTGGCAGTCTCCAGGAAG 198
 QY 61 LysArgCysCysProAspThrCysGlyLysCysLeuAspProValAspThrProAsn 80
 DB 199 AAGAGATGTGTCTGACACTTGGGCATCAATGCTGCTGCTGTGACACCCCAAC 258
 QY 81 ProThrArgArgLysProGlyLysCysProValThrTyrGlnCysLeuMetLeuAsn 100
 DB 259 CCAACAAGGAGGAGCCTGGGAAGTGCCTGAGTACTTATGGCAATGTTTGTATGCTTAA 318
 QY 101 ProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysMetGly 120
 DB 319 CCCCCCAATTTCTGTGAGTGGATGGCAGTGCAGGCTGACTGAGTGTGATGGGC 378
 QY 121 MetCysGlyLysSerCysValSerProValLysAla 132
 DB 379 ATGTGTGGGAATCTCGTTCGTTCCCTGTGAAAGCT 414

RESULT 8

ABL66679 standard; DNA; 594 BP.

AC ABL66679;

XX 15-MAY-2002 (first entry)

XX Lung cancer related gene sequence SEQ ID NO:5016.

XX Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;

KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;

KW cytostatic; gene therapy; antineoplastic; Wilms' tumour; adenocarcinoma;

XX gene; ds.

OS Homo sapiens.
 XX WO200194629-A2.
 PN 13-DEC-2001.
 PD 30-MAY-2001; 2001WO-US010838.
 XX 05-JUN-2000; 2000US-0209473P.
 PR 05-JUN-2000; 2000US-0209531P.
 PR 18-SEP-2000; 2000US-0231133P.
 PR 18-SEP-2000; 2000US-0233617P.
 PR 20-SEP-2000; 2000US-0234009P.
 PR 20-SEP-2000; 2000US-0234034P.
 PR 22-SEP-2000; 2000US-0234505P.
 PR 22-SEP-2000; 2000US-0234509P.
 PR 22-SEP-2000; 2000US-0234567P.
 PR 25-SEP-2000; 2000US-0234923P.
 PR 25-SEP-2000; 2000US-0234924P.
 PR 25-SEP-2000; 2000US-0235077P.
 PR 25-SEP-2000; 2000US-0235082P.
 PR 25-SEP-2000; 2000US-0235134P.
 PR 25-SEP-2000; 2000US-0235280P.
 PR 26-SEP-2000; 2000US-0235637P.
 PR 27-SEP-2000; 2000US-0235638P.
 PR 27-SEP-2000; 2000US-0235711P.
 PR 27-SEP-2000; 2000US-0235720P.
 PR 27-SEP-2000; 2000US-0235840P.
 PR 27-SEP-2000; 2000US-0235863P.
 PR 28-SEP-2000; 2000US-0236028P.
 PR 28-SEP-2000; 2000US-0236032P.
 PR 28-SEP-2000; 2000US-0236033P.
 PR 28-SEP-2000; 2000US-0236034P.
 PR 28-SEP-2000; 2000US-0236109P.
 PR 28-SEP-2000; 2000US-0236111P.
 PR 28-SEP-2000; 2000US-0236842P.
 PR 29-SEP-2000; 2000US-0236891P.
 PR 02-OCT-2000; 2000US-0237172P.
 PR 02-OCT-2000; 2000US-0237173P.
 PR 02-OCT-2000; 2000US-0237278P.
 PR 02-OCT-2000; 2000US-0237294P.
 PR 02-OCT-2000; 2000US-0237295P.
 PR 02-OCT-2000; 2000US-0237316P.
 PR 03-OCT-2000; 2000US-0237425P.
 PR 03-OCT-2000; 2000US-0237598P.
 PR 03-OCT-2000; 2000US-0237604P.
 PR 03-OCT-2000; 2000US-0237606P.
 PR 03-OCT-2000; 2000US-0237608P.
 PR 01-NOV-2000; 2000US-0244867P.
 PR 01-NOV-2000; 2000US-0245084P.

(AVAL-) AVALON PHARM.

Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
 Soppet DR, Weaver Z;

WPI; 2002-188264/24.

Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.

Claim 1; SEQ ID NO 5016; 44pp; English.

The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is

CC the data collected with respect to the anti-neoplastic agent as a result
CC of M1, and the data is sufficient to convey the chemical structure and/or
CC properties of the agent. M1 can be used in the treatment of cancer such
CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms
CC tumour
XX

SQ Sequence 594 BP; 132 A; 156 C; 155 G; 151 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,08e-58 Length: 594
Score: 762.00 Matches: 132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-613-105-2 (1-132) x ABL66679 (1-594)

Qy 1 MetLysSerSerglyLeuPhePropheLeuValLeuLeuAlaLeuGlyThrLeuAlaPro 20
Db 19 ATGAAGTCCAGCGGCTCTTCCCTTCTGCTGCTTCCCTGGGAACCTCTGGCACCT 78
Qy 21 TrpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProLysLysSer 40
Db 79 TGGGCTGTGGAGGCTCTGGAAAGTCTTCAAGCTGGAGTCTGCTCTCTAGAAATCT 138
Qy 41 AlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAspTrpGlnCysProGlyLys 60
Db 139 GCCAGTGCCTTAGATACAAAGAACTGAGTGCAGAGTGACTGGCAGTGCTCCAGGGAAG 198
Qy 61 LysArgCysCysProAspThrCysGlyLysCysLeuAspProValAspThrProAsn 80
Db 199 AAGAGATGTTGTCTGACACTTGTGGCATCAAAATGCTTGTGACACCCCAAC 258
Qy 81 ProThrArgArgLysProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAsn 100
Db 259 CCAACAGAGGAGGAGCTCGGAAGTGCAGTACTTATGGCCATGTTTGTGCTTAAAC 318
Qy 101 ProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysMetGly 120
Db 319 CCCCCCAATTTCTGTGAGATGGATGGCCAGTGCAGGCGTGACTTGAAGTGTTCATGGC 378
Qy 121 MetCysGlyLysSerCysValSerProValLysAla 132
Db 379 ATGTGTGGGAATCTCTCGTTTCCCTGTGAAGCT 414

RESULT 9

AA517499
ID AA517499 standard; cDNA; 594 BP.

XX
AC AA517499;

XX
DT 26-MAR-2002 (first entry)

XX
DE Human cDNA encoding an Antileukoprotease.

XX Human; ss; antileukoprotease; antiinflammatory; antiasthmatic;
KW anti allergic; inflammatory lung disorder; cancer; thyroid tumour;
KW emphysema; asthma; bronchitis; allergy; ovarian carcinoma;
KW renal cell carcinoma.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 19..417

XX /*tag= a

XX /product= "Antileukoprotease"

XX WO200190421-A2.

XX

PD 29-NOV-2001.

XX 25-MAY-2001; 2001WO-US017211.

XX 25-MAY-2000; 2000US-0207104P.

XX (CURA-) CURAGEN CORP.

PA Rastelli L, Smithson G;

XX WPI; 2002-106211/14.

XX P-PSDB; AAU11763.

DR

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Alignment Scores:

Pred. No.: 2,08e-58 Length: 594
Score: 762.00 Matches: 132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-613-105-2 (1-132) x AA517499 (1-594)

Qy 1 MetLysSerSerglyLeuPhePropheLeuValLeuLeuAlaLeuGlyThrLeuAlaPro 20

Db 19 ATGAAGTCCAGCGGCTCTTCCCTTCTGCTGCTTCCCTGGGAACCTCTGGCACCT 78

Qy 21 TrpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProLysLysSer 40

Db 79 TGGGCTGTGGAGGCTCTGGAAGTCTTCAAGCTGGAGTCTGCTCTCTAGAAATCT 138

Qy 41 AlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAspTrpGlnCysProGlyLys 60

Db 139 GCCAGTGCCTTAGATACAAAGAACTGAGTGCAGAGTGACTGGCAGTGCTCCAGGGAAG 198

Qy 61 LysArgCysCysProAspThrCysGlyLysLysCysLeuAspProValAspThrProAsn 80

Db 199 AAGAGATGTTGTCCTGACACTTGGCATCAAAATGCCCTGGATCCTGTTGACACCCCAAC 258
 Qy 81 ProThrArgArgLysProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAen 100
 Db 259 CCAACAAGGAGGAAGCCTGGGAAGTGCCTGAGTGCCTATGTCCTGCAATGTTGATGCTTAAC 318
 Qy 101 ProProAenPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysMetGly 120
 Db 319 CCCCCCAATTTCTGTGAGATGGATGGCCAGTGCAGTGAAGCGTGACTTGAAGTGTTCATGGGC 378
 Qy 121 MetCysGlyLysSerCysValSerProValLysAala 132
 Db 379 ATGTGTGGGAATCCTCGCTTCCCTGTGAAAGCT 414
 RESULT 10
 ABT11084
 ID ABT11084 standard; cDNA; 594 BP.
 AC ABT11084;
 XX
 XX
 DT 04-DEC-2002 (first entry)
 XX
 XX Human breast cancer associated coding sequence SEQ ID NO: 1218.
 DE Human; breast specific gene; breast cancer; differential expression;
 KW cytosstatic; gene therapy; gene; ss.
 KW Homo sapiens.
 OS
 XX
 PN WO200259271-A2.
 XX
 PD 01-AUG-2002.
 XX
 XX 25-JAN-2002; 2002WO-US002176.
 XX
 PR 25-JAN-2001; 2001US-0263757P.
 PR 25-APR-2001; 2001US-0286090P.
 PR 23-MAY-2001; 2001US-0292517P.
 XX
 XX (GENE-) GENE LOGIC INC.
 PA
 XX Orr MS, Nation M, Diggins JC, Zeng W;
 PI
 XX WPI; 2002-674803/72.
 XX
 XX Diagnosing breast cancer in a patient comprises detecting the level of
 PT gene expression in cell or tissue samples, where a differential gene
 PT expression is indicative of breast cancer.
 XX
 XX Claim 1; SEQ ID NO 1218; 260pp + Sequence Listing; English.
 PS
 XX The present invention relates to methods of diagnosing breast cancer in a
 CC patient, which comprise detecting the level of expression in a tissue
 CC sample of two or more genes selected from those shown in ABT09867-
 CC ABT1112, where a differential expression of the genes indicates breast
 CC cancer. The methods are useful in diagnosing, treating, detecting the
 CC progression, and in monitoring treatment of breast cancer in patients.
 CC The methods are also useful as a screening tool for agents that modulate
 CC the onset or progression of breast cancer. The breast cancer genes may be
 CC used as diagnostic markers for the prediction or identification of the
 CC malignant state of breast tissue, for confirming the type and progression
 CC of cancer, and for drug screening and assays. The present sequence is a
 CC coding sequence of the invention. Note: The sequence data for this patent
 CC did not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub.published_pct_sequences
 XX
 SQ Sequence 594 BP; 132 A; 156 C; 155 G; 151 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2.08e-58 Length: 594

Score: 762.00 Matches: 132

Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-613-105-2 (1-132) x ABT11084 (1-594)

Qy 1 MetLysSerSerGlyLeuPheProPheLeuValLeuLeuAlaLeuGlyThrLeuAlaPro 20
 Db 19 ATGAAGTCAGCGCCCTCTTCCCTTCTCTGGTGTCTGTTGCCCTGGGAACCTGGCACCT 78
 Qy 21 TrpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProProLysLysSer 40
 Db 79 TGGGCTGTGGAAGCTCTGGAAGTCTTCAAAAGCTGGAGTCTGTCTCTCTAAGAAATCT 138
 Qy 41 AlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAspTrpGlnCysProGlyLys 60
 Db 139 GCCCAGTGCCTTAGATACAAAGAACCTGAGTGCAGAGTGACTGGCAGTGCTCCAGGGAAG 198
 Qy 61 LysArgCysCysProAspThrCysGlyLysLysCysLeuAspProValAspThrProAen 80
 Db 199 AAGAGATGTTGCTCTGACACTTGTGGCATCAAAATGCCCTGGATCCTGTTGACACCCCAAC 258
 Qy 81 ProThrArgArgLysProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAen 100
 Db 259 CCAACAAGGAGGAAGCCTGGGAAGTGCCTGAGTGCCTATGTCCTGTTGATGCTTAAC 318
 Qy 101 ProProAenPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGly 120
 Db 319 CCCCCCAATTTCTGTGAGATGGATGGCCAGTGCAGCGTGACTTGAAGTGTTCATGGGC 378
 Qy 121 MetCysGlyLysSerCysValSerProValLysAala 132
 Db 379 ATGTGTGGGAATCCTCGCTTCCCTGTGAAAGCT 414

RESULT 11

ABZ34724
 ID ABZ34724 standard; cDNA; 594 BP.

XX ABZ34724;

XX ABZ34724;

XX 04-FEB-2003 (first entry)

XX Coding sequence SEQ ID 82, upregulated in osteogenesis.

XX Osteopathic; osteogenesis modulator; gene therapy; osteogenesis;

XX osteoporosis; bone disease; downregulator; human; ss.

XX Homo sapiens.

XX WO200281745-A2.

XX 17-OCT-2002.

XX 05-APR-2002; 2002WO-IB002211.

XX 05-APR-2001; 2001US-0281400P.

XX (AVET) AVENTIS PHARMA SA.

XX Garcia T, Roman Roman S, Baron R, Call K, Theilhaber J;

XX Connolly T, Jackson A, Bushnell SE, Rawadi G;

XX WPI; 2003-058567/05.

XX Novel isolated nucleic acid upregulated/downregulated in osteogenesis,
 PT useful for bone disease therapy in subject.

XX Claim 26; Page 116; 237pp; English.

XX The present invention relates to novel nucleotide sequences, which are

CC differentially expressed in models of osteogenesis upon being put in
 CC contact with a stimulator of osteogenesis. The present sequence is one

PR 31-DEC-2001; 2001US-0344903P.
 PR 17-APR-2002; 2002US-0373288P.
 PR 15-MAY-2002; 2002US-0380981P.
 PR 17-MAY-2002; 2002US-0381495P.
 PR 28-MAY-2002; 2002US-0383534P.
 PR 28-MAY-2002; 2002US-0383744P.
 PR 29-MAY-2002; 2002US-0383829P.
 PR 29-MAY-2002; 2002US-0384024P.
 PR 07-AUG-2002; 2002US-0401788P.
 PR 26-AUG-2002; 2002US-0406353P.
 PR 31-OCT-2002; 2002US-00401788.
 PR 02-DEC-2002; 2002US-00406353.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Alsbrook JP, Anderson DW, Boldog FL, Burgess CE, Chillakuru RA;
 PI Edinger SR, Gerlach VL, Gorman L, Gould-Rothberg BE, Guo X;
 PI Jeffers ME, Ji W, Li L, Malyankar UM, Miller CE, Murphy R;
 PI Patturajan M, Peyman JA, Rastelli L, Rieger DK, Shenoy SG;
 PI Smithson G, Starling G, Taupier RJ, Voss EZ, Zhong H, Zhong M;
 XX
 DR WPI; 2003-513974/48.
 DR P-PSDB; ADE95612.
 XX
 XX New NOVX polypeptides and nucleic acids, useful for preventing or
 PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
 PT atherosclerosis or diabetes, and in chromosome mapping, tissue typing or
 PT pharmacogenomics.
 XX
 PS Claim 20; SEQ ID NO 143; 211pp; English.
 XX
 CC This invention relates to novel NOVX proteins, and the DNA sequence which
 CC encode them, having properties related to stimulation of biochemical or
 CC physiological responses in a cell, a tissue, an organ or an organism.
 CC Compounds which modulate the proteins of the invention may have cardiant,
 CC antiatherosclerotic, hypotensive, cytostatic, anorectic, antirheumatic,
 CC antiarthritic, antidiabetic, nephrotropic, dermatological,
 CC immunosuppressive, anti-HIV, antiinflammatory, neuroprotective,
 CC neotropic, antipsoriatic, antiparkinsonian, antistomatitic, neuroleptic,
 CC antidepressant, antiallergic or gynaecological activities. The DNA
 CC sequences of the invention may be useful for gene therapy whilst the
 CC protein sequences may allow the development of a vaccine. The protein is
 CC useful in the manufacture of a medicament for treating a syndrome
 CC associated with a human disease. The invention may be useful in
 CC diagnosing, treating or preventing NOVX-associated disorders, for example
 CC cardiomyopathy, atherosclerosis, hypertension, cancer, obesity,
 CC rheumatoid arthritis, diabetes, glomerulonephritis, psoriasis, skin
 CC disorders, AIDS, inflammation, multiple sclerosis, Alzheimer's disease,
 CC Parkinson's disease, asthma, schizophrenia, depression, allergies or
 CC fertility disorders. The nucleic acids may further be used as
 CC hybridisation probes, in chromosome mapping, tissue typing, preventive
 CC medicine, and pharmacogenomics. The present sequence is the cDNA sequence
 CC which encodes the human NOVX27b protein of the invention.
 XX
 SQ Sequence 594 BP; 132 A; 156 C; 155 G; 151 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 2.08e-58 Length: 594
 Score: 762.00 Matches: 132
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0

US-10-613-105-2 (1-132) x ADE95611 (1-594)

QY 1 MetLysSerSerGlyLeuPheProPheLeuValLeuLeuAlaLeuGlyThrLeuAlaPro 20
 DB 19 ATGAAGTCCAGCGGCTCTCCCTTCTGGTGTGCTGGCTGGAACTCTGGACCT 78
 QY 21 TrpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProProLysLysSer 40
 DB 79 TGGGCTGTGAAGGCTCTGGAAGTCTTCAAAGCTGGAGTCTGTCTCTCTTAAGAAATCT 138

QY 41 AlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAspThrGlnCysProGlyLys 60
 DB 139 GCCAGTGCTCTAGATACAGAAACCTGAGTGCAGAGTACTGGCAGTGTCCAGGAG 198
 QY 61 LysArgCysCysProAspThrCysGlyIleLysCysLeuAspProValAspThrProAsn 80
 DB 199 AAGAGATGTTCTCTGACACTTGTGGCATCAATGCTGGATCCTGTGACACCCCAAAC 258
 QY 81 ProThrArgArgLysProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAsn 100
 DB 259 CCAACAAGGAGGAGGAGCTGGGAAGTCCCAAGTACTTATGGCCAAATGTTTGATGCTTAAAC 318
 QY 101 ProProAsnPheCysGluMetAspGlyGlnCysLysLysAspLeuLysCysCysMetGly 120
 DB 319 CCCCCCAATTTCTGTGAGATGGATGCCAGTGCAGCGTGAAGTGTTCATGGGC 378
 QY 121 MetCysGlyLysSerCysValSerProValLysAla 132
 DB 379 ATGTGTGGGAATCCTGCGTTCCTCCCTGTGAAAGCT 414
 RESULT 15
 ADF81611
 ID ADF81611 standard; DNA; 594 BP.
 AC ADF81611;
 XX 26-FEB-2004 (first entry)
 DT
 XX
 DE Leukaemia-related DNA sequence #2167.
 KW Cytostatic; Gene therapy; leukaemia; ss.
 XX Unidentified.
 OS
 PN WO2003039443-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 04-NOV-2002; 2002WO-EP012303.
 PR
 PR 05-NOV-2001; 2001EP-00126244.
 PR 30-APR-2002; 2002EP-00009758.
 XX
 PA (DEK-) DEUT KREBSFORSCHUNGSZENTRUM.
 PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
 PA (HAFE/) HAFERLACH T.
 PA (SCHO/) SCHOCH C.
 PA (KERN/) KERN W.
 XX
 PI Haferlach T, Schoch C, Kern W, Kohlmann A, Schnittger S, Dugas M;
 PI Ellis R, Brors B, Mergenthaler S;
 XX
 DR WPI; 2003-505037/47.
 XX
 PT Determining the subtype of leukemia cells and whether a patient sample
 PT contains leukemia cells or other cells, useful for treating leukemia,
 PT comprises determining the expression profile of a group of markers in a
 PT patient sample.
 PS Disclosure; SEQ ID NO 2167; 2938pp; English.
 XX
 CC The present invention relates to a method (M1) for determining the
 CC subtype of leukaemia cells and whether a patient sample contains
 CC leukaemia cells. The method comprises determining the expression profile
 CC of a group of markers in a patient sample. The method is useful for
 CC determining the presence of leukaemia cells, its types or subtypes, and
 CC for the preparation of a medicament for treating leukaemia.
 XX
 SQ Sequence 594 BP; 132 A; 156 C; 155 G; 151 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 2.08e-58 Length: 594

CC polynucleotide probes comprising a sequence selected from one of the 1499
CC sequences mentioned in the specification. The combination is useful as an
CC array element in a microarray for monitoring the expression of a number
CC of target polynucleotides. The microarray is particularly useful in the
CC diagnosis and treatment of cancer and immunopathology and neuropathology.
CC The microarray is useful in diagnostics and treatment regimens, drug
CC discovery and development, toxicological and carcinogenicity studies,
CC forensic and pharmacogenomics. The microarray is also useful for
CC monitoring progression of diseases and for developing sophisticated
CC profiles for the effects of currently available therapeutic drugs. The
CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs
CC and genomic fragments and in research and diagnostic applications. The
CC array can detect changes in expression in a large number of genes coding
CC for different signalling pathway populations which can be used to diagnose
CC various diseases including cancer e.g. adenocarcinoma and leukaemia,
CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
CC and Parkinson's disease. The present sequence represents a polynucleotide
CC probe of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=06500938B1
XX
SQ Sequence 594 BP; 132 A; 156 C; 155 G; 151 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,086-58 Length: 594
Score: 762.00 Matches: 132
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps:

US-10-613-105-2 (1-132) x ACA56673 (1-594)

Qy 1 MetLysSerSerGlyLeuPheProPheLeuValLeuLeuAlaLeuGlyThrLeuAlaPro 20
Db 19 ATGAAGTCCAGCGGCTCTTCCCTCTCTGGTGCTGCTTCCCTGGGAACTCTGGCACT 78
Qy 21 TrpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProLysLysSer 40
Db 79 TGGGCTGTGGAGGCTCTGGAAGTCTTCAAAGCTGGAGTCTGTCTCTTAAGAAATCT 138
Qy 41 AlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAspTyrGlnCysLeuMetLeuAsn 60
Db 139 GCCAGTGCCTTAGATACAAAGAACTGAGTCCAGAGTGAAGTCTTATGGCCAAATGTTGATGCTTAAAC 198
Qy 61 LysArgCysCysProAspThrCysGlyLysLysCysLeuAspProValAspThrProAsn 80
Db 199 AAGAGATGTTGCTGACACTTGTGGCATCAATGCTGGATCTGTTGACACCCCAAC 258
Qy 81 ProThrArgArgLysProGlyLysCysProValThrTyrGlnCysLeuMetLeuAsn 100
Db 259 CCAACAAGGAGGAGGCTTGGGAAGTCCCTTCAAAGCTGGAGTCTGTCTTGAACCCCAAC 318
Qy 101 ProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGly 120
Db 319 CCCCCCAATTTCTGTGAGATGAGTGGCCAGTGCACAGCTGACTTGAAGTGTGTGATGGGC 378
Qy 121 MetCysGlyLysSerCysValSerProValLysAla 132
Db 379 ATGTGTGGGAAATCTTCGCTTTTCCCTGTGAAAGCT 414

RESULT 16
ACA56673
ID ID ATGTGTGGGAAATCTTCGCTTTTCCCTGTGAAAGCT 414
XX
AC ACA56673;
XX
DT 06-JUN-2003 (first entry)
XX
DE Human signalling pathway polynucleotide probe SEQ ID NO 1271.
XX
KW Human; probe; ss; array element; Parkinson's disease;
KW signalling pathway population; cancer; adenocarcinoma; leukaemia;
KW immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
XX
OS Homo sapiens.
XX
PN US6500938-B1.
XX
PD 31-DEC-2002.
XX
PF 30-JAN-1998; 98US-00016434.
XX
PR 30-JAN-1998; 98US-00016434.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Au-Young J, Seilhamer JU;
XX
DR WPI; 2003-352189/33.
XX
PT Combination of polynucleotide probes, useful as array elements in a
PT microarray for monitoring the expression of a number of target
PT polynucleotides.
XX
PS Claim 1; SEQ ID NO 1271; 65pp; English.
XX
KW The invention relates to a combination which, comprises a number of

Score: 762.00 Matches: 132
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps:

US-10-613-105-2 (1-132) x ADF81611 (1-594)

Qy 1 MetLysSerSerGlyLeuPheProPheLeuValLeuLeuAlaLeuGlyThrLeuAlaPro 20
Db 19 ATGAAGTCCAGCGGCTCTTCCCTTCTGGTGCTGCTTGGCTGGGAACTCTGGCACT 78
Qy 21 TrpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProLysLysSer 40
Db 79 TGGGCTGTGGAGGCTCTGGAAGTCTTCAAAGCTGGAGTCTGTCTTCTTAAGAAATCT 138
Qy 41 AlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAspTyrGlnCysProGlyLys 60
Db 139 GCCAGTGCCTTAGATACAAAGAACTGAGTCCAGAGTGAAGTCTTATGGCCAAATGTTGATGCTTAAAC 198
Qy 61 LysArgCysCysProAspThrCysGlyLysLysCysLeuAspProValAspThrProAsn 80
Db 199 AAGAGATGTTGCTGACACTTGTGGCATCAATGCTGGATCTGTTGACACCCCAAC 258
Qy 81 ProThrArgArgLysProGlyLysCysProValThrTyrGlnCysLeuMetLeuAsn 100
Db 259 CCAACAAGGAGGAGGCTTGGGAAGTCCCTTCAAAGCTGGAGTCTGTCTTGAACCCCAAC 318
Qy 101 ProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGly 120
Db 319 CCCCCCAATTTCTGTGAGATGAGTGGCCAGTGCACAGCTGACTTGAAGTGTGTGATGGGC 378
Qy 121 MetCysGlyLysSerCysValSerProValLysAla 132
Db 379 ATGTGTGGGAAATCTTCGCTTTTCCCTGTGAAAGCT 414

RESULT 16
ACA56673
ID ID ATGTGTGGGAAATCTTCGCTTTTCCCTGTGAAAGCT 414
XX
AC ACA56673;
XX
DT 06-JUN-2003 (first entry)
XX
DE Human signalling pathway polynucleotide probe SEQ ID NO 1271.
XX
KW Human; probe; ss; array element; Parkinson's disease;
KW signalling pathway population; cancer; adenocarcinoma; leukaemia;
KW immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
XX
OS Homo sapiens.
XX
PN US6500938-B1.
XX
PD 31-DEC-2002.
XX
PF 30-JAN-1998; 98US-00016434.
XX
PR 30-JAN-1998; 98US-00016434.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Au-Young J, Seilhamer JU;
XX
DR WPI; 2003-352189/33.
XX
PT Combination of polynucleotide probes, useful as array elements in a
PT microarray for monitoring the expression of a number of target
PT polynucleotides.
XX
PS Claim 1; SEQ ID NO 1271; 65pp; English.
XX
KW The invention relates to a combination which, comprises a number of


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XX SQ Sequence 594 BP; 132 A; 156 C; 155 G; 151 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 2,08e-58 Length: 594
Score: 762.00 Matches: 132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US-10-613-105-2 (1-132) x ADP65640 (1-594)
QY 1 MetLysSerSerGlyLeuPheProPheLeuValLeuAlaLeuGlyThrLeuAlaPro 20
DB 19 ATGAAGTCCAGCGGCTCTTCCCTTCTGGTGTCTGTCCTGGAACTCTGGCACCT 78
QY 21 TrpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProProlsLysSer 40
DB 79 TGGGCTGTGGAGGCTCTGGAAGTCTTCAAGTCTGGAGTCTGCTCTCTAAGAAATCT 138
QY 41 AlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAspTrpGlnCysProGlyLys 60
DB 139 GCCCAGTGCCTTAGATACAGAAACCTGAGTGCAGAGTCTGCGAGTCTCCAGGGAAG 198
QY 61 LysArgCysCysProAspThrCysGlyLysLysCysLeuAspProValAspThrProAsn 80
DB 199 AAGAGATGTTGCTCCTGACACTTGTGGCATCAAAATGCTGGATCTGTTGACACCCCAAC 258
QY 81 ProThrArgArgLysProGlyLysCysProValThrTyrGlnCysLeuMetLeuAsn 100
DB 259 CCAACAGGAGGAGGAGCTGGAGAGTGGCCAGTCACTATGCCCACATGTTGATGCTTAAC 318
QY 101 ProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysMetGly 120
DB 319 CCCCCCAATTTCTGTGAGATGGATGGCCAGTGCAGGCTGACTGAAGTGTTCATGGGC 378

RESULT 19
AD156469
ID AD156469 standard; DNA; 594 BP.
XX AC AD156469;
XX AC AD156469;
XX DT 22-APR-2004 (first entry)
XX DE Human polynucleotide probe #1271.
XX KW Human; probe; ss; receptor-like polypeptide; transducing polypeptide;
XX KW effector-like polypeptide; cancer; immunopathology; neuropathology;
XX KW drug development; toxicology; carcinogenicity;
XX KW signalling pathway polypeptide; adrenal gland; bladder; bone;
XX KW bone marrow; brain; breast; cervix; tumour; immunopathology; AIDS;
XX KW diabetes; pancreatitis; osteoporosis; ulcerative colitis; neuropathology;
XX KW dementia; amnesia; epilepsy; Alzheimer's disease; depression.
XX OS Homo sapiens.
XX PN US2004010136-A1.
XX PD 15-JAN-2004.
XX PF 26-NOV-2002; 2002US-00305720.
XX PR 30-JAN-1998; 98US-00016434.
XX PA (INCY-) INCYTE GENOMICS INC.
XX PI Au-Young J, Seilhamer JJ;
XX

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DR MPI; 2004-090520/09.
XX New composition comprising polynucleotide probes, useful as array
PT elements in a microarray for monitoring the expression of target
PT polynucleotides or purifying a subpopulation of mRNAs, cDNA, or genomic
PT fragments.
XX Claim 6; SEQ ID NO 1271; 73pp; English.
XX The invention relates to a composition of polynucleotide probes
CC comprising first polynucleotide probes comprising at least a portion of a
CC gene encoding a receptor-like polypeptide, second polynucleotide probes
CC comprising at least a portion of a gene encoding a transducing
CC polypeptide and third polynucleotide probes comprising at least a portion
CC of a gene encoding an effector-like polypeptide. The probes of the
CC composition are useful as array elements in a microarray for monitoring
CC the expression of target polynucleotides. The microarray is useful in the
CC diagnosis and treatment of cancer, an immunopathology or a
CC neuropathology. It can also be used for drug discovery and development,
CC toxicological and carcinogenicity studies, forensics or pharmacogenomics.
CC Microarrays can also be used for monitoring the progression of diseases
CC that may be associated with the altered expression of signalling pathway
CC polypeptides. The composition can also be used to purify a subpopulation
CC of mRNAs, cDNAs, or genomic fragments in a sample. The expression profile
CC is also useful for the diagnosis and treatment of cancer, e.g. cancers of
CC the adrenal gland, bladder, bone, bone marrow, brain, breast or cervix,
CC an immunopathology, e.g. AIDS, diabetes, pancreatitis, osteoporosis or
CC ulcerative colitis, or a neuropathology, e.g. dementia, amnesia,
CC epilepsy, Alzheimer's disease or depression. This sequence represents a
CC human polynucleotide probe of the invention. Note: The sequence data for
CC this patent did not form part of the printed specification but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html.
XX SQ Sequence 594 BP; 132 A; 156 C; 155 G; 151 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,08e-58 Length: 594
Score: 762.00 Matches: 132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-10-613-105-2 (1-132) x AD156469 (1-594)
QY 1 MetLysSerSerGlyLeuPheProPheLeuValLeuAlaLeuGlyThrLeuAlaPro 20
DB 19 ATGAAGTCCAGCGGCTCTTCCCTTCTGGTGTCTGTCCTGGAACTCTGGCACCT 78
QY 21 TrpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProProlsLysSer 40
DB 79 TGGGCTGTGGAGGCTCTGGAAGTCTTCAAGTCTGGAGTCTGCTCTCTAAGAAATCT 138
QY 41 AlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAspTrpGlnCysProGlyLys 60
DB 139 GCCCAGTGCCTTAGATACAGAAACCTGAGTGCAGAGTCTGCGAGTCTCCAGGGAAG 198
QY 61 LysArgCysCysProAspThrCysGlyLysLysCysLeuAspProValAspThrProAsn 80
DB 199 AAGAGATGTTGCTCCTGACACTTGTGGCATCAAAATGCTGGATCTGTTGACACCCCAAC 258
QY 81 ProThrArgArgLysProGlyLysCysProValThrTyrGlnCysLeuMetLeuAsn 100
DB 259 CCAACAGGAGGAGGAGCTGGAGAGTGGCCAGTCACTATGCCCACATGTTGATGCTTAAC 318
QY 101 ProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysMetGly 120
DB 319 CCCCCCAATTTCTGTGAGATGGATGGCCAGTGCAGGCTGACTGAAGTGTTCATGGGC 378

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CC in diagnosing ovarian cancer and in identifying and using agents and/or
CC targets that inhibit ovarian cancer. The nucleic acid molecule,
CC polypeptide and the antibody may also be used in detecting ovarian
CC cancers, monitoring and early detection of relapse following treatment,
CC monitoring response to therapy, selecting patients for post-operative
CC chemotherapy or radiation therapy, in selecting mode of therapy,
CC determining tumour prognosis, early detection of pre-cancerous lesions,
CC and as vaccines. This sequence corresponds to one of the nucleic acids
CC used for the detection method of the invention.

XX
SQ Sequence 598 BP; 134 A; 157 C; 156 G; 151 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2.1e-58 Length: 598
Score: 762.00 Matches: 132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-613-105-2 (1-132) x ADB80589 (1-598)

QY 1 MetLysSerSerGlyLeuPheProPheLeuValLeuAlaLeuGlyThrLeuAlaPro 20
DB 23 ATGAAGTCCAGCGCCCTCTCCCTTCTGGTGTCTGCTGGGAACTCTGGCACCT 82
QY 21 TrpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProLysLysSer 40
DB 83 TGGGCTGTGGAGGCTCTGGAAAGTCTCTCAAGCTGGAGTCTGCTCTCTAAGAAATCT 142
QY 41 AlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAspTrpGlnCysProGlyLys 60
DB 143 GCCCAGTGCCTTAGATACAAAGAAACCTGAGTGGCAGAGTCACTGGCAGTCTCCAGGGAAG 202
QY 61 LysArgCysCysProAspThrCysGlyLysCysLeuAspProValAspThrProAsn 80
DB 203 AAGAGATGTTGCTCGACATCTGGGCATCAAAATGCTGGATCTGTGTGACACCCCAAC 262
QY 81 ProThrArgArgLysProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAsn 100
DB 263 CCAACAAGGAGGAAGCTCTGGAGTGGCCAGTCACTATGCCCAATGTTGATGCTTAAC 322
QY 101 ProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysMetGly 120
DB 323 CCCCCCAATTTCTGTGAGATGGATGGCCAGTCAAGCGTGACCTGAAGTGTTCATGGGC 382
QY 121 MetCysGlyLysSerCysValSerProValLysAla 132
DB 383 ATGTGTGGGAATCTCTCGCTTCCCTGTGAAAGCT 418

RESULT 22

ADP65076

ID ADP65076 standard; DNA; 598 BP.

XX

AC ADP65076;

XX

12-AUG-2004 (first entry)

XX

Human secretory leukocyte protease inhibitor DNA sequence.

XX

autoimmune disease; arthritis; gene expression analysis;

XX

rheumatoid arthritis; collagen-induced; immunosuppressive; anti-rheumatic;

XX

antiarthritis; osteopathic; antigout; antiinflammatory; dermatological;

XX

immunomodulatory; lupus; ankylosing spondylitis; fibrositis;

XX

fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;

XX

immune; ds; human.

XX

Homo sapiens.

XX

W02003072827-A1.

XX

04-SEP-2003.

XX

PD

PF 31-OCT-2002; 2002WO-US035433.

XX

PR 31-OCT-2001; 2001US-0336220P.

XX

PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.

XX

PI Hirsch R, Thorton SL;

XX

WP1; 2003-712740/67.

DR

DR GENBANK; NM_003064.

XX

Diagnosing and analyzing autoimmune disease using gene expression

PT profiles and microarray technology, useful for diagnosing and treating

PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and

gout.

XX

Disclosure; Page: 56pp; English.

XX

The invention relates to a novel method for diagnosing and analysing

CC autoimmune disease or arthritides. The method comprises obtaining a

CC patient sample containing mRNA, analysing gene expression using the mRNA

CC that results in a gene expression signature of the mRNA, and using that

CC gene expression signature to diagnose or analyse the autoimmune disease

CC or arthritides in the patient, where gene expression of at least 50% of

CC the genes correlates with that of the gene signature. The invention

CC further comprises: a treatment of rheumatoid arthritis; identification of

CC genes for targeting in the treatment of rheumatoid arthritis in a mammal

CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an

CC array or gene chip, specific for rheumatoid arthritis; diagnosis or

CC analyses of autoimmune disease or rheumatoid arthritis; screening the

CC efficacy of a candidate drug in vitro for the treatment of collagen-

CC induced arthritis; and reducing the symptoms associated with collagen-

CC induced arthritis. The compositions of the invention have the following

CC activities: immunosuppressive, antirheumatic, antiarthritis, osteopathic,

CC antigout, antiinflammatory, dermatological, and immunomodulatory. The

CC methods and compositions of the present invention are useful for

CC diagnosing and treating autoimmune disease or arthritides, such as

CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,

CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an

CC immune disease caused by an infectious agent. This polynucleotide

CC represents a DNA sequence relating to the genes used in the analysis and

CC treatment of autoimmune diseases or arthritides. Note: This sequence is

CC not shown in the specification. It has been supplied in an electronic

CC format from WIPO.

XX

SQ Sequence 598 BP; 134 A; 157 C; 156 G; 151 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2.1e-58 Length: 598
Score: 762.00 Matches: 132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US-10-613-105-2 (1-132) x ADP65076 (1-598)

QY 1 MetLysSerSerGlyLeuPheProPheLeuValLeuAlaLeuGlyThrLeuAlaPro 20
DB 23 ATGAAGTCCAGCGCCCTCTCCCTTCTGGTGTCTGCTGGGAACTCTGGCACCT 82
QY 21 TrpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProLysLysSer 40
DB 83 TGGGCTGTGGAGGCTCTGGAAAGTCTCTCAAGCTGGAGTCTGCTCTCTAAGAAATCT 142
QY 41 AlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAspTrpGlnCysProGlyLys 60
DB 143 GCCCAGTGCCTTAGATACAAAGAAACCTGAGTGGCAGAGTCACTGGCAGTCTCCAGGGAAG 202
QY 61 LysArgCysCysProAspThrCysGlyLysCysLeuAspProValAspThrProAsn 80
DB 203 AAGAGATGTTGCTCGACATCTGGGCATCAAAATGCTGGATCTGTGTGACACCCCAAC 262

QY 81 ProThrArgArgLysProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAen 100
 |||||
 Db 263 CCAACAAGAGGAGAGCTGGAGTGCCTGACCTTATGGCCAAATGTTTGATGCTTAAC 322
 |||||
 QY 101 ProProAenPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGly 120
 |||||
 Db 323 CCCCCCAATTTCTGTGATGGATGGCGCAGTGCAGTGCAGGCGTGACTTGAAGTGTGATGGGC 382
 |||||
 QY 121 MetCysGlyLysSerCysValSerProValLysAla 132
 |||||
 Db 383 ATGTGTGGAAATCCTCGCTTCCCTGTGAAAGCT 418
 |||||

RESULT 23

ADL26771

ID ADL26771 standard; cDNA; 598 BP.

XX AC ADL26771;

XX DT 03-JUN-2004 (first entry)

XX DE Human SLPI encoding cDNA SEQ ID NO:25.

XX KW ovarian cancer; ovarian cancer-associated transcript; cytostatic;
 XX KW gene therapy; human; secretory leukocyte protease inhibitor;
 XX KW chromosome 20; gene; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 XX FT CDS 23..421
 XX FT /*tag= a
 XX FT /product= "SLPI"

XX PN W02004022778-A1.

XX PD 18-MAR-2004.

XX PF 05-SEP-2003; 2003WO-AU001166.

XX PR 05-SEP-2002; 2002AU-00951346.

XX PS (GARV-) GARVAN INST MEDICAL RES.

XX PI Sutherland R, Henshall S, O'Brien P;

XX PT WPI; 2004-315574/29.

XX DR P-PSDB; ADL26772.

XX DT Use of genes and proteins for diagnosing ovarian cancer and/or a
 XX PT likelihood for survival or recurrence of the disease.

XX PS Claim 2; SEQ ID NO 25; 447pp; English.

XX CC The present invention describes a method for the use of genes and
 CC proteins for diagnosing ovarian cancer and/or a likelihood for survival
 CC or recurrence of the disease, where the expression of genes and proteins
 CC is up-regulated and down-regulated or associated with the occurrence or
 CC recurrence of a specific cancer sub-type. Also described: (1) detecting
 CC an ovarian cancer-associated transcript in a biological sample; (2)
 CC (3) detecting an ovarian cancer in a human or animal subject being tested;
 CC (4) monitoring the efficacy of a therapeutic treatment of ovarian
 CC cancer; (5) determining the likelihood of survival of a subject suffering
 CC from an ovarian cancer; and (6) an assay device for use in the diagnosis
 CC or prognosis of ovarian cancer comprising polynucleotides or antibodies
 CC immobilised to a solid phase, where each of the polynucleotides consists
 CC of a gene given in the specification and each of the antibodies binds to
 CC a polypeptide also given in the specification; and identifying a
 CC candidate compound for the treatment of ovarian cancer. An ovarian cancer
 CC -associated sequence has cytostatic activity, and can be used in gene
 CC therapy. An ovarian cancer-associated polynucleotide, vector, polypeptide
 CC or antibody can be used for the diagnosis or prognosis of ovarian cancer
 CC or for the preparation of a medicament for the treatment of ovarian

CC cancer. The ovarian cancer that is diagnosed is an epithelial ovarian
 CC cancer selected from serous ovarian cancer, non-invasive ovarian cancer,
 CC mixed phenotype ovarian cancer, mucinous ovarian cancer, endometrial
 CC ovarian cancer, clear cell ovarian cancer, papillary serous ovarian
 CC cancer, Brenner cell or undifferentiated adenocarcinoma. The present
 CC sequence encodes human secretory leukocyte protease inhibitor (SLPI),
 CC which is located on chromosome 20 and is used in the exemplification of
 CC the present invention.

XX SQ Sequence 598 BP; 134 A; 157 C; 156 G; 151 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,1e-58 Length: 598
 Score: 762.00 Matches: 132
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 12 Gaps: 0

US-10-613-105-2 (1-132) x ADL26771 (1-598)

QY 1 MetLysSerSerGlyLeuPheProPheLeuValLeuLeuAlaLeuGlyThrLeuAlaPro 20
 |||||

Db 23 ATGAAGTCCAGCGGCTCTTCCCTTCTGGTGCTGCTTCCCTGGAACTCTGGCACCT 82
 |||||

QY 21 TtpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProProLysLysSer 40
 |||||

Db 83 TGGGCTGTGGAGGCTCTGGAAAGTCTTCAAGCTGGAGTCTGCTCTCTAAGAAATCT 142
 |||||

QY 41 AlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAspTrpGlnCysProGlyLys 60
 |||||

Db 143 GCCCAGTCTCTAGATACAAAGAACTGAGTGCAGAGTACTGGCAGTGTCCAGGGAAG 202
 |||||

QY 61 LysArgCysCysProAspThrCysGlyLysCysLeuAspProValAspThrProAsn 80
 |||||

Db 203 AAGAGATGTTGTCTGACACTTTGTGGCATCAAAATGCTGGATCTCTTGACACCCCAAC 262
 |||||

QY 81 ProThrArgArgLysProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAen 100
 |||||

Db 263 CCAACAAGAGGAGGAGCTGGGAAGTGCACGAGTACTATGGCCAAATGTTTGATGCTTAAC 322
 |||||

QY 101 ProProAenPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGly 120
 |||||

Db 323 CCCCCCAATTTCTGTGAGATGGATGGCCAGTGCAGCTGACTTGAAGTGTTCATGGGC 382
 |||||

QY 121 MetCysGlyLysSerCysValSerProValLysAla 132
 |||||

Db 383 ATGTGTGGAAATCCTCGCTTCCCTGTGAAAGCT 418
 |||||

RESULT 24

ADN03925

ID ADN03925 standard; cDNA; 598 BP.

XX AC ADN03925;

XX DT 01-JUL-2004 (first entry)

XX DE Antipsoriatic cDNA sequence #162.

XX KW ds; gene; antipsoriatic; gene therapy; psoriasis; diagnosis.

XX OS Homo sapiens.

XX PN W02004028479-A2.

XX PD 08-APR-2004.

XX PF 25-SEP-2003; 2003WO-US030907.

XX PR 25-SEP-2002; 2002US-0414006P.

XX PA (GETH) GENENTECH INC.

XX XX


```

QY 121 MetCysGlyLysSerCysValSerProValIysAla 132
DB 374 ATGTGTGGGAATCTCGCTTCCCTGTGAAAGCT 409

RESULT 26
ID AAH57451
XX AAH57451 standard; cDNA; 636 BP.
AC AAH57451;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human lung cell specific cDNA sequence SEQ ID NO:291.
XX
KW Human; tissue specific; diagnosis; brain; heart; skeletal muscle; lung;
KW liver; uterus; ovary; stomach; intestine; kidney; pancreas; ss;
KW metabolic disease; developmental disease; cytostatic; immunomodulatory;
KW neuroprotective; gene therapy; cancer; immunopathology; neuropathology.
XX
OS Homo sapiens.
XX
PN W0200132927-A2.
XX
PD 10-MAY-2001.
XX
PF 02-NOV-2000; 2000WO-US030396.
XX
PR 04-NOV-1999; 99US-0163508P.
XX
PA (INCYTE) INCYTE GENOMICS INC.
XX
PI Sornasse T, Seilhamer JJ, Watson GA;
XX
DR WPI; 2001-291057/30.
XX
PT New cell and tissue specific polynucleotides useful for diagnosis,
PT prognosis or monitoring of treatments for disorders where the gene is
PT associated with a cancer, immunopathology or neuropathology.
XX
PS Claim 1; Page 217; 327pp; English.
XX
CC AAH57161 to AAH57576 represent cell and tissue specific polynucleotide
CC sequences (I). (I) can have cytostatic, immunomodulatory and
CC neuroprotective activities, and can be used in gene therapy. (I) and
CC proteins (II) encoded by then are used in high throughput screening
CC assays to select DNA molecules, RNA molecules, peptide nucleic acids,
CC mimetics, peptides, proteins, agonists, antagonists, antibodies or their
CC fragments, immunoglobulins, inhibitors, drug compounds and pharmaceutical
CC agents. Expression of (I) in a sample indicates the differentiation of
CC embryonic stem cells into a tissue selected from brain, heart, kidney,
CC liver, lung, skeletal muscle or pancreatic tissues. (I) and (II) are used
CC to produce an expression profile that defines a metabolic or
CC developmental process, treatment, condition, disease or disorder. The
CC gene profile can be used for diagnosis, prognosis or monitoring of
CC treatments and for investigating a predisposition to a disorder where the
CC gene is associated with a cancer, immunopathology or neuropathology
XX
SQ Sequence 636 BP; 160 A; 159 C; 163 G; 154 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.26e-58 Length: 636
Score: 762.00 Matches: 132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-613-105-2 (1-132) x AAH57451 (1-636)

QY 1 MetLysSerGlyLeuPheProPheLeuValLeuLeuAlaLeuGlyThrLeuAlaPro 20
DB 56 ATGAAGTCCAGCGGCTCTTCCCTTCTGCTGCTTGCCTGTGGAAGCTCTGGCACCT 115

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QY 21 TrpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProProlYsLysSer 40
DB 116 TGGGCTGTGGAGGCTCTGGAAAGCTCTTCAAGCTGGAGTCTGTCTCTCTAAGAAATCT 175

QY 41 AlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAspTyrGlnCysProGlyLys 60
DB 176 GCCCAGTGGCTTAGATACAAGAAACCTGAGTGCAGAGTGACTGGCAGTGTCTCCAGGGAAG 235

QY 61 LysArgCysCysProAspThrCysGlyLysLysCysLeuAspProValAspThrProAsn 80
DB 236 AAGAGATGTGTCTGACACCTTGTGGCATCAATGCTGGATCTCTGTGACACCCCAAC 295

QY 81 ProThrArgArgLysProGlyLysCysProValThrTyrGlnCysLeuMetLeuAsn 100
DB 296 CCACACAGAGAGGAGGCTGGGAAGTCCCAAGTACTTATGGCCCAATGTTGATGCTTAAC 355

QY 101 ProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGly 120
DB 356 CCCCCCAATTTCTGTGAGATGGATGGCAGTGCCAGCGTGACTTGAAGTGTTCATGGGC 415

QY 121 MetCysGlyLysSerCysValSerProValIysAla 132
DB 416 ATGTGTGGGAATCTCGCTTCCCTGTGAAAGCT 451

RESULT 27
ADL62375
ID ADL62375 standard; DNA; 1084 BP.
XX
AC ADL62375;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human ovarian cancer DNA marker #20587.
XX
KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX
OS Homo sapiens.
XX
PN W0200170979-A2.
XX
PD 27-SEP-2001.
XX
PR 21-MAR-2001; 2001WO-US009126.
XX
PR 21-MAR-2000; 2000US-0191031P.
PR 23-MAY-2000; 2000US-0207124P.
PR 15-JUN-2000; 2000US-0211940P.
PR 07-JUL-2000; 2000US-0216820P.
PR 25-JUL-2000; 2000US-0220661P.
PR 21-DEC-2000; 2000US-0257672P.
XX
(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
Lee J, Lillie J;
XX
WPI; 2001-611502/70.
XX
PT Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
PT cancer cells as compared to their normal non-cancerous ovarian cells are
PT used to characterize stage, grade, histological type of ovarian cancer.
XX
PS Disclosure; SEQ ID NO 20587; 106pp; English.
XX
CC The invention relates to nucleic acid markers which are overexpressed in
CC ovarian cancer cells as compared to their expression in normal (i.e. non-
CC cancerous) ovarian cells. The invention also relates to polypeptides
CC encoded by the markers, antibodies that selectively bind to the
CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
CC of developing ovarian cancer involving inhibiting expression of a gene
CC corresponding to a marker of the invention and a method of treating a
CC patient afflicted with ovarian cancer comprising providing to cells of
CC the patient an antisense oligonucleotide complementary to a marker of the

```


CC transmembrane protein-like; NOV12a-12c show homology to beta-neoendorphin
CC -dynorphin precursor. The present sequence encodes a NOVX polypeptide of
CC the invention.

XX SQ Sequence 594 BP; 132 A; 157 C; 155 G; 150 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1,06e-57 Length: 594
Score: 754.00 Matches: 131
Percent Similarity: 99.24% Conservatism: 0
Best Local Similarity: 99.24% Mismatches: 1
Query Match: 98.95% Indels: 0
DB: 12 Gaps: 0

US-10-613-105-2 (1-132) x ADL57140 (1-594)

QY 1 MetLysSerSerGlyLeuPheProPheLeuValLeuLeuAlaLeuGlyThrLeuAlaPro 20
DB 19 ATGAAGTCCAGCGGCTCTCCCTTCTGGTGTCTGCTGGCTGGGAACCTCTGGCACCT 78
QY 21 TTPAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProProLysLysSer 40
DB 79 TGGGCTGTGGAAGCTCTGGAAGTCTTCAAAGCTGGAGTCTGTCTCTTAAGAAATCT 138
QY 41 AlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAspTrpGlnCysProGlyLys 60
DB 139 GCCAGTGCCTTAGATACAGAAACCTGAGTGCAGAGTCACTGGCAGTGTCCAGGGAAG 198
QY 61 LysArgCysCysProAspThrCysGlyIleLysCysLeuAspProValAspThrProAsn 80
DB 199 AAGAGATGTTGCTGACACTTGTGGCATCAAAATGCTGGATCTGTGTGACACCCCAAC 258
QY 81 ProThrArgArgLysProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAsn 100
DB 259 CCAACAGAGAGAGAGCTGCGAAGTGCCTGAGTGCCTGATGCTATGGCAATGTTGATGCTTAAC 318
QY 101 ProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGly 120
DB 319 CCCCCCAATTTCTGTGAGATGGATGGCCAGTGCAGGCGTGCATGAGTGTGCATGGGC 378
QY 121 MetCysGlyLysSerCysValSerProValLysAla 132
DB 379 ATGTGTGGGAATCTCGCTTTCCCTGTGAAAGCT 414

RESULT 31

ID ADL57142 standard; DNA; 594 BP.

XX AC ADL57142;

XX DT 03-JUN-2004 (first entry)

XX DE Human NOV8b gene SEQ ID NO:87.

XX ds; gene; human; antidiabetic; anorectic; cardiant; hypotensive;
KW antiarteriosclerotic; anorectic; virucide; antibacterial; fungicide;
KW protozoacide; nootropic; neuroprotective; antiparkinsonian;
KW anticonvulsant; osteopathic; antiarthritic; antiinflammatory;
KW dermatological; antiasthmatic; antilipemic; gene therapy;
KW fibroblast growth factor receptor 4; FGFR4;
KW complement factor I precursor; matrix metalloproteinase-15 precursor;
KW MDC3; T-lymphocyte surface antigen Ly-9 precursor;
KW alpha-2 macroglobulin-like polypeptide variant;
KW antileukoprotease 1 precursor; LIV-1; nuclear hormone receptor NOR-1;
KW transmembrane protein-like; beta-neoendorphin-dynorphin precursor.

XX OS Homo sapiens.

XX PH Key Location/Qualifiers

XX FT CDS 19..417

XX FT /*tag= a

XX

PN WO2004022723-A2.

XX PD 18-MAR-2004.

XX PF 09-SEP-2003; 2003WO-US028141.

XX PF 09-SEP-2002; 2002US-0409145P.

PR 10-SEP-2002; 2002US-0409544P.

PR 12-SEP-2002; 2002US-0410320P.

PR 15-SEP-2002; 2002US-0411060P.

PR 23-SEP-2002; 2002US-0412766P.

PR 23-SEP-2002; 2002US-0412825P.

PR 24-SEP-2002; 2002US-0412767P.

PR 25-SEP-2002; 2002US-0413342P.

PR 30-SEP-2002; 2002US-0414832P.

XX (CURA-) CURAGEN CORP.

PA Zhong M, Guo X, Anderson DW, Ort T, Padigaru M, Rieger DK;

PI P-PSDB; ADL57143.

XX WPI: 2004-315567/29.
DR P-PSDB; ADL57143.
XX New isolated NOVX polypeptides and polynucleotides, useful for
PT preventing, diagnosing or treating NOVX-associated disorders, e.g.
PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
PT asthma, or infections.

XX Claim 17; SEQ ID NO 87; 214pp; English.

XX The invention relates to a novel isolated polypeptide (NOVX) comprising a
PS mature form of any of the 37 amino acid sequences fully defined in the
CC specification. A polypeptide of the invention has antidiabetic,
CC anorectic, cardiant, hypotensive, antiarteriosclerotic, anorectic,
CC virucide, antibacterial, fungicide, protozoacide, nootropic,
CC neuroprotective, antiparkinsonian, anticonvulsant, osteopathic,
CC antiarthritic, antiinflammatory, dermatological, antiasthmatic, and
CC antilipemic activity. A polynucleotide of the invention may have a use
CC in gene therapy. The polypeptides, nucleic acid molecules and antibodies
CC are useful in the manufacture of a medicament for treating a syndrome
CC associated with a human disease, preferably a NOVX-associated disorder.
CC The nucleic acid molecules, polypeptides and antibodies are useful for
CC treating, preventing or diagnosing diseases such as metabolic disorders,
CC diabetes, obesity, infectious diseases (viral, bacterial, fungal,
CC helminthic, and protozoal), anorexia, cancer, cardiovascular diseases
CC (hypertension, atherosclerosis), neurodegenerative disorders, Alzheimer's
CC disease, Parkinson's disease, epilepsy, immune disorders
CC (osteoarthritis), haematopoietic disorders, inflammatory skin disorders,
CC asthma, and various dyslipidaemias. The nucleic acids and polypeptides
CC may also be used as targets for the identification of small molecules
CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell
CC proliferation, haematopoiesis, wound healing and angiogenesis, in gene
CC therapy, in generation of antibodies that bind immunospecifically to NOVX
CC substances for use in therapeutic or diagnostic methods. The nucleic
CC acids are further used as hybridisation probes, in chromosome mapping,
CC tissue typing, preventive medicine, and pharmacogenomics. The NOVX
CC polypeptides of the invention show homology to certain known human
CC proteins: NOV1a-1t show homology to fibroblast growth factor receptor 4
CC (FGFR4); NOV2a shows homology to complement factor I precursor; NOV3a
CC shows homology to matrix metalloproteinase-15 precursor; NOV4a shows
CC homology to MDC3; NOV5a-5c show homology to T-lymphocyte surface antigen
CC Ly-9 precursor; NOV6a-6m show homology to fibroblast growth factor-21
CC (FGF-21); NOV7a-7c show homology to alpha-2 macroglobulin-like
CC polypeptide variant; NOV8a-8g show homology to antileukoprotease 1
CC precursor; NOV9a-9i show homology to LIV-1 protein; NOV10a shows homology
CC to nuclear hormone receptor NOR-1; NOV11a-11j show homology to
CC transmembrane protein-like; NOV12a-12c show homology to beta-neoendorphin
CC -dynorphin precursor. The present sequence encodes a NOVX polypeptide of
CC the invention.

XX SQ Sequence 594 BP; 132 A; 157 C; 155 G; 150 T; 0 U; 0 Other;

Alignment Scores:

XX 09-SEP-2002; 2002US-0409145P.
PR 10-SEP-2002; 2002US-0409544P.
PR 12-SEP-2002; 2002US-0410320P.
PR 16-SEP-2002; 2002US-0411060P.
PR 23-SEP-2002; 2002US-0412766P.
PR 23-SEP-2002; 2002US-0412825P.
PR 24-SEP-2002; 2002US-0412767P.
PR 25-SEP-2002; 2002US-0413342P.
PR 30-SEP-2002; 2002US-0414832P.
XX (CURA-) CURAGEN CORP.
XX
XX Zhong M, Guo X, Anderson DW, Ort T, Padigaru M, Rieger DK;
XX WPI: 2004-315567/29.
XX P-PSDB; ADL57151.
XX
XX New isolated NOVX polypeptides and polynucleotides, useful for
PT preventing, diagnosing or treating NOVX-associated disorders, e.g.
PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
PT asthma, or infections.
XX
XX Claim 17; SEQ ID NO 95; 214pp; English.
XX
XX The invention relates to a novel isolated polypeptide (NOVX) comprising a
CC mature form of any of the 37 amino acid sequences fully defined in the
CC specification. A polypeptide of the invention has antidiabetic,
CC anorectic, cardiac, hypotensive, antiarteriosclerotic, anorectic,
CC virucide, antibacterial, fungicide, protozoacide, neurotropic,
CC neuroprotective, antiparkinsonian, anticonvulsant, osteopathic,
CC antiarthritic, antiinflammatory, dermatological, antiasthmatic, and
CC antilipaemic activity. A polynucleotide of the invention may have a use
CC in gene therapy. The polypeptide, nucleic acid molecules and antibodies
CC are useful in the manufacture of a medicament for treating a syndrome
CC associated with a human disease, preferably a NOVX-associated disorder.
CC The nucleic acid molecules, polypeptides and antibodies are useful for
CC treating, preventing or diagnosing diseases such as metabolic disorders,
CC diabetes, obesity, infectious diseases (viral, bacterial, fungal,
CC helminthic, and protozoal), anorexia, cancer, cardiovascular diseases
CC (hypertension, atherosclerosis), neurodegenerative disorders, Alzheimer's
CC disease, Parkinson's disease, epilepsy, immune disorders
CC (osteoarthritis), haematopoietic disorders, inflammatory skin disorders,
CC asthma, and various dyslipidaemias. The nucleic acids and polypeptides
CC may also be used as targets for the identification of small molecules
CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell
CC proliferation, haematopoiesis, wound healing and angiogenesis, in gene
CC therapy, in generation of antibodies that bind immunospecifically to NOVX
CC substances for use in therapeutic or diagnostic methods. The nucleic
CC acids are further used as hybridisation probes, in chromosome mapping,
CC tissue typing, preventive medicine, and pharmacogenomics. The NOVX
CC polypeptides of the invention show homology to certain known human
CC proteins: NOV1a-1t show homology to fibroblast growth factor receptor 4
CC (FGFR4); NOV2a shows homology to complement factor I precursor; NOV3a
CC shows homology to matrix metalloproteinase-15 precursor; NOV4a shows
CC homology to MDC3; NOV5a-5c show homology to T-lymphocyte surface antigen
CC Ly-9 precursor; NOV6a-6m show homology to fibroblast growth factor-21
CC (FGF-21); NOV7a-7c show homology to alpha-2 macroglobulin-like
CC polypeptide variant; NOV8a-8g show homology to antileukoproteinase 1
CC precursor; NOV9a-9i show homology to LIV-1 protein; NOV10a shows homology
CC to nuclear hormone receptor NOR-1; NOV11a-11j show homology to
CC transmembrane protein-like; NOV12a-12c show homology to beta-neoendorphin
CC -dynorphin precursor. The present sequence encodes a NOVX polypeptide of
CC the invention.
XX
XX SQ Sequence 594 BP; 132 A; 156 C; 155 G; 146 T; 0 U; 5 Other;

Alignment Scores:
Pred. No.: 5,86e-55 Length: 594
Score: 723.00 Matches: 127
Percent Similarity: 96.21% Conservative: 0
Best Local Similarity: 96.21% Mismatches: 5
Query Match: 94.88% Indels: 0

DB: 12 Gaps: 0
US-10-613-105-2 (1-132) x ADL57150 (1-594)
Qy 1 MetLysSerSerGlyLeuPheProPheLeuValLeuLeuAlaLeuGlyThrLeuAlaPro 20
Db 19 ATGAAGTCCAGCGCCCTCTYCCCTTCTCGTGGTCYCGCTTGCCCTGGGAATCTGGCACCT 78
Qy 21 TTPAlaValIdgluglySerGlyLysSerPheLysAlaGlyValCysProProLysLysSer 40
Db 79 TGGGCTGTGGAAGGCTCTGGAAGTCTTCAAAGTGGAGTCTGTCTCTCTTAAGAAATCT 138
Qy 41 AlaGlnCysLeuArgTyrLysLysProGluCysGlnSerHapTrpGlnCysProGlyLys 60
Db 139 GCCCAGTGCCTTAGATACAAAGAACTGAGYGGCAGAGTGACTGGCAGTGTCCAGGGAAG 198
Qy 61 LysArgCysCysProHapThrCysGlyLysLysCysLeuAspProValAspThrProAan 80
Db 199 AAGAGATGTTGCTCTGACACTTGTGGCATCAATGCTGGATCCTGTTGACACCCCAAC 258
Qy 81 ProThrArgArgLysProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAan 100
Db 259 CCACACAGGAGGAGGAGCTGGGAAGTGCCAGTGACTTATGCCCAATGTTTGATGCTTAAC 318
Qy 101 ProProAanPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGly 120
Db 319 CCCCCCAATTTCTGTGAGATGGATGCCAGTGCAAGCGTGACTTGAAGTGTTCATGGC 378
Qy 121 MetCysGlyLysSerCysValSerProValLysAla 132
Db 379 ATGTGTGGGAATCCYCGCTTCCCTGTGAAAGCT 414
RESULT 35
AAL60894
ID AAL60894 standard; cDNA; 605 BP.
XX AAL60894;
XX AC
XX DT 03-SEP-2003 (first entry)
XX DE Human secretory leukocyte proteinase inhibitor variant (Sepin) cDNA.
XX KW Human; forensic analysis; chromosome marker; organelle-specific marker;
KW novel-related disorder; neurological disorder; gene therapy; neurotropic;
KW neuroprotective; secretory leukocyte proteinase inhibitor; inhibitor;
KW variant; Sepin; gene; ss.
XX OS Homo sapiens.
XX OS Synthetic.
XX PH Key Location/Qualifiers
FT 5'UTR 1..21 /tag= a
FT CDS 22..363 /tag= b
FT /product= "Human Sepin protein"
FT sig_peptide 22..96 /tag= c
FT mat_peptide 97..360 /tag= d
FT /product= "Human mature Sepin protein"
FT 3'UTR 364..605 /tag= e
FT polyA_signal 565..570 /tag= f
FT polyA_site 590..605 /tag= g
XX WO2003046180-A2.
XX PD 05-JUN-2003.
XX PF 25-NOV-2002; 2002WO-BP013210.


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Db      346 CTGATCCTGTTGACACCCCAACCCCAAGGAGGAGCCTGGGAAGTGCCTCCAGTACT 287.
Qy      93  TyrGlnCysLeuMetLeuAsnProProAsnPheCysGluMetAspGlyGlnCysLys 112
      286  TATGCCCAATGTTGATGCTTAACCCCCCAATTTCTGTGAGATGGATGCCAGTCAAG 227
Qy      113 ArgAspLeuLysCysCysMetGlyMetCysGlyLysSerCysValSerProValLysAla 132
      226 CGTGACTGAAGTGTTCATGGGCATGTGTGGGAATCCTGCGTTTCCCTGTGAAAGCT 167
RESULT 37
AX16271
ID      AX16271 standard; DNA; 460 BP.
XX
AC      AX16271;
DT      20-MAR-2003 (revised)
DT      19-APR-1999 (first entry)
XX
DE      DNA sequence of ompA-SLPI.
XX
KW      Serine protease inhibitor; human; emphysema; arthritis; periodontitis;
KW      muscular dystrophy; tumour invasion; glomerulonephritis; sepsis;
KW      acute leukemia; ds.
XX
OS      Homo sapiens.
OS      Synthetic.
XX
PN      US5871956-A.
XX
PD      16-FEB-1999.
XX
PF      22-JUL-1994; 94US-00279056.
XX
PR      06-DEC-1984; 84US-00678822.
PR      29-JUL-1986; 86US-00890526.
PR      03-SEP-1986; 86US-00903471.
PR      30-MAR-1987; 87US-00031846.
PR      06-AUG-1990; 90US-00563832.
XX
PA      (AMGE-) AMGEN INC.
XX
PI      Stetler GL, Bandyopadhyay PK, Eisenberg SP, Thompson RC;
XX
XX      WPI; 1999-166640/14.
XX
XX      New DNA sequence encoding mammalian serine protease inhibitor - useful
PT      for recombinantly producing inhibitors with different specificities, and
PT      treating diseases such as emphysema, arthritis, muscular dystrophy, and
PT      tumor invasion.
XX
XX      Example 3; Col 37-38; 37pp; English.
XX
CC      The present invention describes a DNA sequence (A) encoding an analogue
CC      of a mammalian serine protease inhibitor (B). The DNA sequences and
CC      recombinant methods allow manufacture of a class of inhibitors of e.g.
CC      cathepsin G, elastase, and trypsin, with different specificities. The
CC      recombinant serine protease product can be directed to act
CC      intracellularly or extracellularly and is useful in treating conditions
CC      caused by a disturbance in the native protease/protease inhibitor balance
CC      such as emphysema, arthritis, glomerulonephritis, periodontitis, muscular
CC      dystrophy, tumour invasion, sepsis, and acute leukemia. (A) allows (B) to
CC      be recombinantly produced in sufficient quantities and purities so as to
CC      provide economical pharmaceutical compositions. (B) is resistant to heat,
CC      acid, and a variety of proteolytic enzymes, is thermodynamically stable
CC      in extracellular conditions, and exhibits a high degree of self assembly
CC      forming an active tertiary structure in the absence of biochemical
CC      stimuli. The present sequence represents the DNA sequence of ompA-SLPI.
CC      (Updated on 20-MAR-2003 to correct PR field.)
XX
XX      Sequence 460 BP; 123 A; 114 C; 125 G; 98 T; 0 U; 0 Other;
SQ

```

Alignment Scores:

```

Pred. No.: 3,41e-48 Length: 460
Score: 645.00 Matches: 112
Percent Similarity: 88.64% Conservative: 5
Best Local Similarity: 84.85% Mismatches: 11
Query Match: 84.65% Indels: 4
DB: 2 Gaps: 1

US-10-613-105-2 (1-132) x AX16271 (1-460)
Qy      1  MetLysSerSerGlyLeuPheProPheLeuValLeuLeuAlaLeuGlyThrLeuAlaPro 20
      62  ATGAAAAGACAGCTATCGCATCGCAGTGGCACTGGCTGGTTTCGTACCGTAGCG--- 118
Qy      21  TrpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProProLysLysSer 40
      119  -----CAGGCCTCTGGTAAAGCTTCAAAGCTTCAAGCTGATGCGCGCGGAAAAATCC 169
Qy      41  AlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAspTrpGlnCysProGlyLys 60
      170  GCCAGTGTTCTGCGGTACAAAAACCGGAATGCCAGTCCGACATGGCAGTCCCGGGTAAA 229
Qy      61  LysArgCysCysProAspThrCysGlyLysCysLeuAspProValAspThrProAsn 80
      230  AAACGTTGTGCCCGGACACCTCGGCGATCAATGCTGGATCGGTTGATACCCGAAC 289
Qy      81  ProThrArgArgLysProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAsn 100
      290  CCGACTCGTCGAAAACCGGGTAAATGCCCGTAACCTATATGCCAGTGTCTGTGATGCTGAAC 349
Qy      101  ProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGly 120
      350  CCGCGAACTTCTGCGAAATGGACGCCAGTGTAAACGAGATCTGAAATCTGTATGGGT 409
Qy      121  MetCysGlyLysSerCysValSerProValLysAla 132
      410  ATGTGGGCAAACTTGTGTTTCCCGGTAAAAAGCA 445

RESULT 38
AAC97622
ID      AAC97622 standard; DNA; 460 BP.
XX
AC      AAC97622;
XX
XX      27-FEB-2001 (first entry)
XX
DE      DNA encoding OmpA secretory leukocyte protease inhibitor.
XX
XX      Serine protease inhibitor; cytostatic; anti-inflammatory; arthritis;
KW      protease mediated tissue destruction; emphysema; glomerulonephritis;
KW      periodontitis; muscular dystrophy; tumour invasion; chymotrypsin;
KW      elastase; ds.
XX
OS      Synthetic.
XX
XX      US6132990-A.
XX
XX      17-OCT-2000.
XX
XX      07-JUN-1991; 91US-00712354.
XX
XX      06-DEC-1984; 84US-00678822.
XX      02-DEC-1985; 85US-00803471.
XX      29-JUL-1986; 86US-00890526.
XX      30-MAR-1987; 87US-00031846.
XX      04-AUG-1987; 87US-00082962.
XX      03-JAN-1989; 89US-00293042.
XX
XX      (AMGE-) AMGEN BOULDER INC.
XX
XX      Bandyopadhyay PK, Eisenberg SP, Stetler GL, Thompson RC;
XX      WPI; 2000-678667/66.
XX
XX

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PT New serine protease inhibitors and DNA sequences for treating a protease-mediated condition or tissue destruction e.g. emphysema or tumor invasion

PT and for recombinant production of inhibitors.

XX Example 3; Col 37-38; 47pp; English.

XX This invention relates to new purified and isolated mammalian serine protease inhibitor proteins which comprise at least 8 cysteine residues and no more than 107 amino acids. The protease inhibitors are capable of inhibiting chymotrypsin and elastase. Sequences AAC97526 - AAC97534, AAC97574 - AAC97581 and AAC97614 - AAC97641 represent DNA encoding the protease inhibitors of the invention, and include oligonucleotide sequences used in the isolation and characterisation of the proteins. Primers AAC97535 - AAC97573 and AAC95582 - AAC97613 are used in the construction of DNA encoding the protease inhibitors. Peptide sequences AAC95098 - AAC95122 represent the protease inhibitors of the invention and various other peptides used in the isolation of the protease inhibitors. The protease inhibitors have cytostatic and anti-inflammatory activity. The serine protease inhibitor protein is useful for treating a protease-mediated condition, which includes protease mediated tissue destruction, e.g. emphysema, arthritis, glomerulonephritis, periodontitis, muscular dystrophy or tumour invasion. It is also useful for modulating protease activity. The DNAs are useful for producing the proteins, especially by recombinant methods

SQ Sequence 460 BP; 123 A; 114 C; 125 G; 98 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3,41e-48 Length: 460
Score: 645.00 Matches: 112
Percent Similarity: 88.64% Conservative: 5
Best Local Similarity: 84.85% Mismatches: 11
Query Match: 84.65% Indels: 4
DB: 3 Gaps: 1

US-10-613-105-2 (1-132) x AAC97622 (1-460)

QY 1 MetLysSerGlyLeuPheProPheLeuValLeuAlaLeuGlyThrLeuAlaPro 20
DB 62 ATGAAAGACAGCTATCGGATCGGACGCTGGCTGGTTTCGTACCGTAGCG--- 118
QY 21 TrpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProProLysLysSer 40
DB 119 -----CAGGCCTCTGGTAAAGCTTCAAAGCTGGCTATGCGCGCGGAAATATCC 169
QY 41 AlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAspTrpGlnCysProGlyLys 60
DB 170 GCGCAGTGTCTGCGGTACAAAACCGGAATGCCAGTCCGACTGGCAGTCCCGGGTAA 229
QY 61 LysArgCysCysProAspThrCysGlyLysCysLeuAspProValAspThrProAsn 80
DB 230 AAAGTTGTTCGCGGACACTCGGGCATCAATGCTGGATCGGTTGTATACCCGGAAC 289
QY 81 ProThrArgArgLysProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAsn 100
DB 290 CCGACTCGTGGAAACCGGGTAAATGCCGTAACCTATGCCAGTGTCTGATGCTGAAC 349
QY 101 ProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGly 120
DB 350 CCGCCGAACCTCTCGAAATGGACGGCGCAGTGTAAACGAGATCTGAAATCTGTATGGGT 409
QY 121 MetCysGlyLysSerCysValSerProValLysAla 132
DB 410 ATGTGCGGCAATCTTGTTTCCCGGTAAAGCA 445

RESULT 39

AAI67582

ID AAI67582 standard; DNA; 460 BP.

XX

AC AAI67582;

XX

DT 11-FEB-2002 (first entry)

XX

DE DNA sequence coding for ompA SLPI.

XX Serine protease inhibitor protein; recombinant; leukocyte elastase;

KW trypsin; secretory leukocyte protease inhibitor; SLPI; ds.

XX Homo sapiens.

OS

XX US6291662-B1.

PN

XX 18-SEP-2001.

PD

XX 22-SEP-1998; 98US-00158085.

PF

XX 05-DEC-1984; 84US-00678222.

PR

XX 02-DEC-1985; 85US-00803471.

PR

XX 29-JUL-1986; 86US-00890526.

PR

XX 30-MAR-1987; 87US-00031846.

PR

XX 06-AUG-1990; 90US-00563832.

PR

XX 22-JUL-1994; 94US-00279056.

XX (AMGE-) AMGEN INC.

XX Bandyopadhyay PK, Eisenberg SP, Stetler GL, Thompson RC;

PI WPI; 2001-637974/73.

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Qy 101 ProProAsnPheCysGluMetAspGlyGlnCysLysHrgAepLeuLysCysCysMetGly 120
Db 350 CCGCCGAACCTCTCGAAATGGACGGCCAGTGTAAACGAGATCTGAAATGCTGTATGGGT 409
Qy 121 MetCysGlyLysSerCysValSerProValLysAla 132
Db 410 ATGTGCGCAAAATCTGTGTTTCCCGGTAAGCA 445
RESULT 40
ABK88025
ID ABK88025 standard; DNA; 1525 BP.
AC ABK88025;
XX
DT 07-OCT-2002 (first entry)
XX
DE DNA sequence encoding rSLAP1 fusion protein.
XX
KW rSLAP1; gene; ds; Alzheimer's disease; tumour angiogenesis; malaria;
KW emphysema; asthma; chronic obstructive pulmonary disease;
KW cystic fibrosis; otitis media; otitis externa; HIV; psoriasis; eczema;
KW human immunodeficiency virus; atopic dermatitis; muscular dystrophy;
KW herpes; ulceration; sepsis; rheumatoid arthritis; periodontal disease;
KW tumour metastasis; osteoporosis; Paget's disease; scleroderma;
KW glomerulonephritis; hypertension.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT RBS 6..8
FT FT /*tag= a
FT FT /standard_name= "Ribosome binding site"
FT FT 9..1520
FT FT /*tag= b
FT FT /product= "rSLAP1 fusion protein"
FT FT 12..1193
FT FT /*tag= c
FT FT /note= "AAT coding region"
FT FT 1194..1196
FT FT /*tag= d
FT FT /note= "linking codon"
FT FT 1197..1517
FT FT /*tag= e
FT FT /note= "SLPI coding region"
XX
PN WO200250287-A2.
XX
XX 27-JUN-2002.
XX
XX 18-DEC-2001; 2001WO-US049256.
XX
XX 18-DEC-2000; 2000US-0256699P.
XX
XX 20-NOV-2001; 2001US-0331966P.
XX
XX (ARRI-) ARRIVA PHARM INC.
XX
XX Barr PJ, Gibson HL, Pemberton P;
XX
XX WPI; 2002-500631/53.
XX
XX P-PSDB; AAU99884.
XX
XX Novel fusion protein useful for inhibiting protease activity associated
XX with a disorder such as emphysema, asthma, comprises a first protease
XX inhibitor comprising alpha 1-antitrypsin and a second protease inhibitor.
XX
XX Example 3; Page 89-90; 134pp; English.
XX
XX This invention relates to a novel fusion protein comprising a first
XX protease inhibitor comprising an alpha1-antitrypsin or its functionally
XX active portion and a second protease inhibitor or its functionally active
XX protein. The fusion proteins of the invention may act as an inhibitor of
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CC protease activity. The fusion protein of the invention is useful for
CC inhibiting protease activity associated with a disorder such as
CC emphysema, asthma, chronic obstructive pulmonary disease, cystic
CC fibrosis, otitis media, otitis externa or HIV infection, or for treating
CC an individual suffering from or at risk for a disease or disorder
CC involving unwanted protease activity. The proteins are useful for
CC treating dermatological diseases such as atopic dermatitis, eczema and
CC psoriasis, in inflammatory responses to viral infection, and for treating
CC herpes infection, corneal or epidermal ulceration, chronic non-healing
CC wounds, sepsis, rheumatoid arthritis, periodontal disease, tumour
CC metastasis and tumour angiogenesis, gastric ulceration, osteoporosis,
CC Paget's disease, glomerulonephritis, scleroderma, malaria, bacterial
CC infection, Alzheimer's disease, hypertension and muscular dystrophy. The
CC present sequence represents the DNA encoding the rSLAP1 fusion protein of
CC the invention
XX
SQ Sequence 1525 BP; 467 A; 287 C; 314 G; 457 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 5.3e-47 Length: 1525
Score: 638.50 Matches: 112
Percent Similarity: 87.97% Conservative: 5
Best Local Similarity: 84.21% Mismatches: 9
Query Match: 83.79% Indels: 7
DB: 6 Gaps: 1
US-10-613-105-2 (1-132) x ABK88025 (1-1525)
Qy 7 PheProPheLeuValLeu-----LeuAlaLeuGlyThrLeuAla 19
Db 1119 TTCGTTTCTGATGATCGAGCAGACACTAAAGCCCATTTGTTGGGTAAAGTTGTC 1178
Qy 20 ProTrpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProProLysLys 39
Db 1179 AACCCAACTCAGAGATGTCGCGAAGTCTTTCAGGCCGGTGTGTTGCCCAAGAAG 1238
Qy 40 SerAlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAspTrpGlnCysProGly 59
Db 1239 TCCGCTCAATGTTTGAGATACAAAGAGCCAGAGATGTCAATCCGACTGGCAATGTCAGGT 1298
Qy 60 LysLysArgCysCysProAspThrCysGlyLysCysLysLeuAspProValAspThrPro 79
Db 1299 AAGAAGAGATGTTGTCAGACACTTGTGGTATCAAGTGTCTAGACCAGTTGACACCCCA 1358
Qy 80 AsnProThrArgArgLysProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeu 99
Db 1359 AACCCAACTAGAGAAAGCCAGCTAAGTGTCCAGTTACTTACCGTCAATGTTGATGTTG 1418
Qy 100 AsnProProAsnPheCysGluMetAspGlyGlnCysLysHrgAepLeuLysCysCysMet 119
Db 1419 AACCCCAAACTCTGTGAATGGACGGTCAATGTAAAGAGAGACTTGAAGTGTGTATG 1478
Qy 120 GlyMetCysGlyLysSerCysValSerProValLysAla 132
Db 1479 GGATATGTGTGTAAGTCTGTGTTTCCCGAGTCAAGGCC 1517
RESULT 41
ABK88016
ID ABK88016 standard; DNA; 321 BP.
XX
AC ABK88016;
XX
DT 07-OCT-2002 (first entry)
XX
DE DNA encoding human secretory leukoprotease inhibitor (SLPI) protein.
XX
KW Secretory leukoprotease inhibitor; human; gene; ds; protease inhibitor;
KW malaria; emphysema; asthma; chronic obstructive pulmonary disease; SLPI;
KW cystic fibrosis; otitis media; otitis externa; HIV; psoriasis; eczema;
KW human immunodeficiency virus; atopic dermatitis; muscular dystrophy;
KW herpes; ulceration; sepsis; rheumatoid arthritis; periodontal disease;
KW tumour metastasis; tumour angiogenesis; osteoporosis; Paget's disease;
KW glomerulonephritis; scleroderma; Alzheimer's disease; hypertension.
```

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX CDS 1..321

XX FT /*tag= a

XX FT /product= "Secretory leukoprotease inhibitor"

XX FT /partial

XX FT /note= "No start or stop codon shown"

XX PN W0200250287-A2.

XX PD 27-JUN-2002.

XX PF 18-DEC-2001; 2001WO-US049256.

XX PR 18-DEC-2000; 2000US-0256699P.

XX PR 20-NOV-2001; 2001US-0331966P.

XX PA (ARRI-) ARRIVA PHARM INC.

XX PI Barr PJ, Gibson HL, Pemberton P;

XX DR WPI; 2002-500631/53.

XX DR P-PSDB; AAU99874.

XX PT Novel fusion protein useful for inhibiting protease activity associated with a disorder such as emphysema, asthma, comprises a first protease inhibitor comprising alpha 1-antitrypsin and a second protease inhibitor.

XX PS Disclosure; Page 32; 134pp; English.

XX CC This invention relates to a novel fusion protein comprising a first protease inhibitor comprising an alpha1-antitrypsin or its functionally active portion and a second protease inhibitor or its functionally active protein. The fusion proteins of the invention may act as an inhibitor of protease activity. The fusion protein of the invention is useful for inhibiting protease activity associated with a disorder such as emphysema, asthma, chronic obstructive pulmonary disease, cystic fibrosis, otitis media, otitis externa or HIV infection, or for treating an individual suffering from or at risk for a disease or disorder involving unwanted protease activity. The proteins are useful for treating dermatological diseases such as atopic dermatitis, eczema and psoriasis, in inflammatory responses to viral infection, and for treating herpes infection, corneal or epidermal ulceration, chronic non-healing wounds, sepsis, rheumatoid arthritis, periodontal disease, tumour metastasis and tumour angiogenesis, gastric ulceration, osteoporosis, Paget's disease, glomerulonephritis, scleroderma, malaria, bacterial infection, Alzheimer's disease, hypertension and muscular dystrophy. The present sequence represents the DNA encoding the human secretory leukoprotease inhibitor used to create the fusion protein of the invention

XX SQ Sequence 321 BP; 92 A; 67 C; 80 G; 82 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1-71e-47	Length:	321
Score:	635.00	Matches:	107
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	83.33%	Indels:	0
DB:	6	Gaps:	0

US-10-613-105-2 (1-132) x ABK88016 (1-321)

Qy 26 SerGlyLysSerPhelysAlaGlyValCysProProlyLysSerAlaGlnCysLeuArg 45

Db 1 TCTGGAAGTCTTCAAGGCGGTTGTGTCCACCAAGAAGTCCGCTCAATGTTTGA 60

Qy 46 TyrlYlYsProGluCysGlnSerAspTyrGlnCysProGlyLysArgCysCysPro 65

Db 61 TACAAGAAGCCAGAAATGTCAATCGACTGGCAATGTCCAGGTAAAGAGATGTTGCCA 120

Qy 66 AspThrCysGlyIleLysCysLeuAspProValAspThrProAsnProThrArgArgLys 85

Db 121 GACACTTGTGGTATCAAGTGTCTAGACCCAGTTGACACCCCAACCACTAGAGAAAG 180

Qy 86 ProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAsnProProAsnPheCys 105

Db 181 CCAGGTAAGTGTCCAGTTACTTACGGTCAATGTTGATGTGAACCCACCAACTTCTGT 240

Qy 106 GluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetClyMetCysGlyLysSer 125

Db 241 GAAATGGACGGTCAATGTAAGAGAGACTTGAAGTGTGTATGGTATGTTGTAAGTCC 300

Qy 126 CysValSerProValLysAla 132

Db 301 TGTGTTTCCCGAGTCAAGGCC 321

RESULT 42

AD895613

ID ADE95613 standard; cDNA; 321 BP.

XX AC ADE95613;

XX DT 12-FEB-2004 (first entry)

XX DE Human NOVX27c protein cDNA sequence.

XX KW NOVX protein; biochemical stimulation; physiological stimulation; cardian; antiarteriosclerotic; hypotensive; cytostatic; anorectic; antirheumatic; antiarthritic; antidiabetic; nephrotoxic; dermatological; immunosuppressive; anti-HIV; antiinflammatory; neuroprotective; neurotropic; antipsoriatic; antiparkinsonian; antiasthmatic; neuroleptic; antidepressant; antiallergic; gynaecological; gene therapy; vaccine; NOVX-associated disorder; cardiomyopathy; atherosclerosis; hypertension; cancer; obesity; rheumatoid arthritis; diabetes; glomerulonephritis; psoriasis; skin disorder; AIDS; inflammation; multiple sclerosis; Alzheimer's disease; Parkinson's disease; asthma; schizoprenia; depression; allergy; fertility disorder; gens; ss; NOVX27c.

XX OS Homo sapiens.

XX WO2003050245-A2.

XX 19-JUN-2003.

XX PF 03-DEC-2002; 2002WO-US038594.

XX PR 05-DEC-2001; 2001US-0336600P.

XX PR 07-DEC-2001; 2001US-0338285P.

XX PR 12-DEC-2001; 2001US-0341346P.

XX PR 17-DEC-2001; 2001US-0341477P.

XX PR 17-DEC-2001; 2001US-0341540P.

XX PR 20-DEC-2001; 2001US-0342592P.

XX PR 27-DEC-2001; 2001US-0344297P.

XX PR 31-DEC-2001; 2001US-0344903P.

XX PR 17-APR-2002; 2002US-0373288P.

XX PR 15-MAY-2002; 2002US-0380981P.

XX PR 17-MAY-2002; 2002US-0381495P.

XX PR 28-MAY-2002; 2002US-0383534P.

XX PR 28-MAY-2002; 2002US-0383744P.

XX PR 29-MAY-2002; 2002US-0383829P.

XX PR 29-MAY-2002; 2002US-0384024P.

XX PR 07-AUG-2002; 2002US-0401788P.

XX PR 26-AUG-2002; 2002US-0406353P.

XX PR 31-OCT-2002; 2002US-00401788.

XX PR 02-DEC-2002; 2002US-00406353.

XX PA (CURA-) CURAGEN CORP.

XX PI Alsobrook JP, Anderson DW, Boldog FL, Burgess CE, Chillakuru RA; Edinger SR, Gerlach VL, Gorman L, Gould-Rothberg BE, Guo X; Jeffers ME, Ji W, Li L, Malyankar UM, Miller CE, Murphy R; Patturajan M, Peyman JA, Rastelli L, Rieger DK, Shenoy SG; Smithson G, Starling G, Taupier RJ, Voess EZ, Zhong H, Zhong M;


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XX WPI; 2003-513974/48.
DR P-PSDB; ADE95614.
XX
XX New NOVX polypeptides and nucleic acids, useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis or diabetes, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
XX Claim 20; SEQ ID NO 145; 211pp; English.
XX
XX This invention relates to novel NOVX proteins, and the DNA sequence which
CC encode them, having properties related to stimulation of biochemical or
CC physiological responses in a cell, a tissue, an organ or an organism.
CC Compounds which modulate the proteins of the invention may have cardiant,
CC antiarteriosclerotic, hypotensive, cytostatic, anorectic, antirheumatic,
CC antiarthritic, antidiabetic, nephrotropic, dermatological,
CC immunosuppressive, anti-HIV, antiinflammatory, neuroprotective,
CC nootropic, antipsoriatic, antiparkinsonian, antiasthmatic, neuroleptic,
CC antidepressant, antiallergic or gynaecological activities. The DNA
CC sequences of the invention may be useful for gene therapy whilst the
CC protein sequences may allow the development of a vaccine. The protein is
CC useful in the manufacture of a medicament for treating a syndrome
CC associated with a human disease. The invention may be useful in
CC diagnosing, treating or preventing NOVX-associated disorders, for example
CC cardiomyopathy, atherosclerosis, hypertension, cancer, obesity,
CC rheumatoid arthritis, diabetes, glomerulonephritis, psoriasis, skin
CC disorders, AIDS, inflammation, multiple sclerosis, Alzheimer's disease,
CC Parkinson's disease, asthma, schizophrenia, depression, allergies or
CC fertility disorders. The nucleic acids may further be used as
CC hybridisation probes, in chromosome mapping, tissue typing, preventive
CC medicine, and pharmacogenomics. The present sequence is the cDNA sequence
CC which encodes the human NOVX27c protein of the invention.
XX
XX Sequence 321 BP; 81 A; 76 C; 87 G; 77 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 1.71e-47 Length: 321
Score: 635.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 83.33% Indels: 0
DB: 10 Gaps: 0
US-10-613-105-2 (1-132) x ADE95613 (1-321)
Qy 26 SerGlyLysSerPheLysAlaGlyValCysProProlLysLysSerAlaGlnCysLeuArg 45
Db 1 TCTGGAAGTGCCTTCAAAAGCTGGAGTCTGCTCCTTAAGAAATCTGCCCAAGTGCCTTAGA 60
Qy 46 TyrLysLysProGluCysGlnSerAspTTPGlnCysProGlyLysLysArgCysCysPro 65
Db 61 TACAGAAACCTGATGCCAGAGTACTGGCAGTGTCCAGGGAAGAGAGATGTTGCTCT 120
Qy 66 AspThrCysGlyLysCysLeuAspProValAspThrProAsnProThrArgArgLys 85
Db 121 GACACTTGTGCATCAATGCCTGGATCTGCTTGAACCCCAACCAAGGAGGAG 180
Qy 86 ProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAsnProProAsnPheCys 105
Db 181 CCTGGGAAGTGCCAGTGACTATGGCCAAATGTTTGTATGCTTAACCCCAATTTCTGT 240
Qy 106 GluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGlyMetCysGlyLysSer 125
Db 241 GAGATGATGCCAGTGCACAGCGTACTTGAAGTGTTCATGGGCATGTGGGAAATCC 300
Qy 126 CysValSerProValLysAla 132
Db 301 TCGCTTTCCCTGTGAAAGCT 321
RESULT 43
AAN60463
ID AAN60463 standard; DNA; 324 BP.
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XX AAN60463;
AC
XX 25-MAR-2003 (revised)
DT 01-JAN-1980 (first entry)
XX
XX Serine protease inhibitor analogue having similar properties to a protein
DE isolated from parotid secretions.
XX
XX Serine protease-inhibitor; parotid; leukocyte-elastase-inhibitor;
KW trypsin-; inhibitor; ss.
KW
XX Synthetic.
OS
XX W08603519-A.
PN
XX 19-JUN-1986.
PD
XX 04-DEC-1985; 85WO-US0002385.
PF
XX 06-DEC-1984; 84US-00678822.
PR
XX 02-DEC-1985; 85US-00803471.
PR
XX (SYND ) SYNERGEN BIOLOGICAL INC.
PA
XX Bandyopadhyay PK, Eisenberg SP, Stetler GL, Thompson RC;
PI WPI; 1986-169458/26.
XX P-PSDB; AAP60562.
DR
XX New synthetic DNA sequences for directing microbial synthesis - for
PT prodn. of single polypeptide chain serine protease inhibitor having
PT leukocyte elastase and trypsin inhibitory sites.
XX
XX Disclosure; Page 14; 59pp; English.
XX
XX The sequence directs synthesis of a single chain polypeptide serine
CC protease-inhibitor, which believed to have at least 2 active sites, 1
CC exhibiting leukocyte-elastase-inhibiting properties and the other
CC exhibiting activity against trypsin. See also AAN60464-69 and AAP60562-
CC 66. (Updated on 25-MAR-2003 to correct PA field.)
XX
XX Sequence 324 BP; 87 A; 85 C; 88 G; 64 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 1.73e-47 Length: 324
Score: 635.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 83.33% Indels: 0
DB: 1 Gaps: 0
US-10-613-105-2 (1-132) x AAN60463 (1-324)
Qy 26 SerGlyLysSerPheLysAlaGlyValCysProProlLysLysSerAlaGlnCysLeuArg 45
Db 1 AGCGGTAAAGAGCTTCAAAAGCTGGCGTATGCCCGCGGAAAAATCCCGCGAGTGTCTCGG 60
Qy 46 TyrLysLysProGluCysGlnSerAspTTPGlnCysProGlyLysLysArgCysCysPro 65
Db 61 TACAAAAAACCGGAATGCCAGTCCGAGTCCGAGTCCGCGGTAATAAACCGTTGTGGCCG 120
Qy 66 AspThrCysGlyLysLysCysLeuAspProValAspThrProAsnProThrArgArgLys 85
Db 121 GACACTTGGCGCATCAAAATGCCCTGGATCCGCTTGATACCCCGAACCCGACTCGTGAANA 180
Qy 86 ProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAsnProProAsnPheCys 105
Db 181 CCGGGTAAATGCCCGGTAACTATGGCCAGTGTCTGATGCTGAACCCCGCGAATCTTCTGC 240
Qy 106 GluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGlyMetCysGlyLysSer 125
Db 241 GAAATGGACGCCAGTGAACGAGATCTGAAATGCTGTATGGGTATGTGCGGCAATCT 300
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QY 126 CysValSerProVallysAla 132
 Db 301 TGTGTTTCCCGGTAAAGCA 321
 RESULT 44
 AAN60464
 ID AAN60464 standard; DNA; 324 BP.
 XX
 AC AAN60464;
 XX
 XX 25-MAR-2003 (revised)
 DT 01-JAN-1980 (first entry)
 XX
 XX Synthetic sequence capable of directing microbial synthesis of a
 DE secretory leukocyte protease-inhibitor.
 XX
 KW Serine protease-inhibitor; parotid; leukocyte-elastase-inhibitor;
 KW trypsin-; inhibitor; ss.
 XX
 OS Synthetic.
 XX
 PN W08603519-A.
 XX
 XX 19-JUN-1986.
 XX
 XX 04-DEC-1985; 85WO-US002385.
 XX
 XX 06-DEC-1984; 84US-00678822.
 PR
 XX 02-DEC-1985; 85US-00803471.
 XX
 XX (SYND) SYNERGEN BIOLOGICAL INC.
 XX
 XX Bandyopadhyay PK, Eisenberg SP, Stetler GL, Thompson RC;
 PI
 XX WPI; 1986-169458/26.
 DR
 DR P-PSDB; AAP60563.
 XX
 XX New synthetic DNA sequences for directing microbial synthesis - for
 PT prodn. of single polypeptide chain serine protease inhibitor having
 PT leukocyte elastase and trypsin inhibitory sites.
 XX
 XX Disclosure; Page 15; 59pp; English.
 PS
 XX The sequence directs synthesis of a secretory leukocyte protease-
 CC inhibitor. See also AAN60463, AAN60465-69 and AAP60562. AAP60564-66.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 324 BP; 86 A; 85 C; 87 G; 66 T; 0 U; 0 Other;
 Alignment Scores: ~ Length: 324
 Pred. No.: 1.73e-47 Matches: 107
 Score: 635.00
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 83.33% Indels: 0
 DB: 1 Gaps: 0
 US-10-613-105-2 (1-132) x AAN60464 (1-324)
 QY 26 SerGlyLysSerPheLysAlaGlyValCysProProLysLysSerAlaGlnCysLeuArg 45
 Db 1 TCTGTTAAAGCTTCAAGCTGGGTATGCCCGCGGAATAATCCGCGAGTGTCTCGG 60
 QY 46 TyrLysLysProGluCysGlnSerAspTrpGlnCysProGlyLysLysArgCysCysPro 65
 Db 61 TACAAAAACCGGAATGCCAGTCCGACTGGCAGTGCCTGCGGTAAACACGTTGTGCGG 120
 QY 66 AspThrCysGlyLysLysCysLeuAspProValAspThrProAsnProThrArgArgLys 85
 Db 121 GACACCTGCGGCATCAATGCTGGATCCGGTGTATACCCGGAACCCGACTCGCGAAA 180
 QY 86 ProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAsnProProAsnPheCys 105

Db 181 CCGGTAATGCCGGTAAACCTATGTCAGTGTCTGATGCTGAACCGCGAATCTTCG 240
 QY 106 GluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetClyMetCysGlyLysSer 125
 Db 241 GAAATGGACGGCCAGTGTAAACGAGATCTGAAATGCTGTATGGGTATGTGCGCAATCT 300
 QY 126 CysValSerProVallysAla 132
 Db 301 TGTGTTTCCCGGTAAAGCA 321
 RESULT 45
 AAX16236
 ID AAX16236 standard; DNA; 324 BP.
 XX
 AC AAX16236;
 XX
 XX 20-MAR-2003 (revised)
 DT 19-APR-1999 (first entry)
 XX
 DE Serine protease inhibitor direct manufacturing DNA sequence (SLPI).
 XX
 KW Serine protease inhibitor; human; emphysema; arthritis; peridontitis;
 KW muscular dystrophy; tumour invasion; glomerulonephritis; sepsis;
 KW acute leukemia; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN US5871956-A.
 XX
 XX 16-FEB-1999.
 XX
 XX 22-JUL-1994; 94US-00279056.
 PF
 XX 06-DEC-1984; 84US-00678822.
 PR
 XX 29-JUL-1986; 86US-00890526.
 PR
 XX 03-SEP-1986; 86US-00903471.
 PR
 XX 30-MAR-1987; 87US-00031846.
 PR
 XX 06-AUG-1990; 90US-00563832.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 XX Stetler GL, Bandyopadhyay PK, Eisenberg SP, Thompson RC;
 PI
 XX WPI; 1999-166640/14.
 DR
 XX New DNA sequence encoding mammalian serine protease inhibitor - useful
 PT for recombinantly producing inhibitors with different specificities and
 PT treating diseases such as emphysema, arthritis, muscular dystrophy, and
 PT tumor invasion.
 XX
 XX Example 2; Col 29; 37pp; English.
 PS
 XX The present invention describes a DNA sequence (A) encoding an analogue
 of a mammalian serine protease inhibitor (B). The DNA sequences and
 CC recombinant methods allow manufacture of a class of inhibitors of e.g.
 CC cathepsin G, elastase, and trypsin, with different specificities. The
 CC recombinant serine protease product can be directed to act
 CC intracellularly or extracellularly and is useful in treating conditions
 CC caused by a disturbance in the native protease/protease inhibitor balance
 CC such as emphysema, arthritis, glomerulonephritis, peridontitis, muscular
 CC dystrophy, tumour invasion, sepsis, and acute leukemia. (A) allows (B) to
 CC be recombinantly produced in sufficient quantities and purities so as to
 CC provide economical pharmaceutical compositions. (B) is resistant to heat,
 CC acid, and a variety of proteolytic enzymes, is thermodynamically stable,
 CC in extracellular conditions, and exhibits a high degree of self assembly
 CC forming an active tertiary structure in the absence of biochemical
 CC stimuli. The present sequence represents a DNA sequence which is used to
 CC direct manufacture of recombinant serine protease inhibitors. (Updated on
 CC 20-MAR-2003 to correct PR field.)
 XX
 SQ Sequence 324 BP; 86 A; 85 C; 87 G; 66 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.73e-47	Length:	324
Score:	635.00	Matches:	107
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	83.33%	Indels:	0
DB:	2	Gaps:	0

US-10-613-105-2 (1-132) x AAX16236 (1-324)

Qy	26	SerGlyLysSerPheLysAlaGlyValCysProProLysLysSerAlaGlnCysLeuArg	45
Db	1	TCTGGTAAAGCTTCAAAGCTGGCGTATGCCCGCGAAAAATCCCGGCAGTGTCTGCGG	60
Qy	46	TyrLysLysProGluCysGlnSerAspTyrGlnCysProGlyLysLysArgCysCysPro	65
Db	61	TACAAAAACCGGANTGCCAGTCCGACTGCGCAGTGGCCGGGTAAAAACGTTGTCGGG	120
Qy	66	AspThrCysGlyLleLysCysLeuAspProValAspThrProAsnProThrArgArgLys	85
Db	121	GACACCTGCGGCATCAATGCCCTGGATCCGTTGATACCCCGAACCGACTCGTCGAAAA	180
Qy	86	ProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAsnProProAsnPheCys	105
Db	181	CCGGTAAATGCCCGGTAAACCTATGGCCAGTGTCTGATGCTGAACCGCGCAACTTCTGC	240
Qy	106	GluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGlyMetCysGlyLysSer	125
Db	241	GAATGGACGGCCAGTGTAAACGAGATCTGAATGCTGTATGGGTATGTCGGCAATCT	300
Qy	126	CysValSerProValLysAla	132
Db	301	TGTGTTTCCCGGTAAAGCA	321

Search completed: October 24, 2004, 04:07:34

Job time : 450 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 24, 2004, 03:15:16 ; Search time 3545 Seconds

(without alignments)
1760.858 Million cell updates/sec

Title: US-10-613-105-2

Perfect score: 762

Sequence: 1 MKSGLFPPFLVLALGTLP.....RDLKCCMGKSCVSPVKA 132

Scoring table:

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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1: gb.ba.*
2: gb.hcg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	762	100.0	399	6	AX302535 Sequence
2	762	100.0	399	9	AF114471 Homo sapi
3	762	100.0	551	6	AX778065 Sequence
4	762	100.0	565	6	I01502 Sequence 3

AX069252 Sequence	565	100.0	762	5
AX04503 Human SLPI	573	100.0	762	6
CQ273731 Sequence	594	100.0	762	7
AR270708 Sequence	594	100.0	762	8
AX328399 Sequence	594	100.0	762	9
AX334507 Sequence	594	100.0	762	10
AX335376 Sequence	594	100.0	762	11
AX577960 Sequence	594	100.0	762	12
AX780010 Sequence	594	100.0	762	13
AX04470 Human mRNA	594	100.0	762	14
BD203743 Human nuc	599	100.0	762	15
AX014898 Sequence	599	100.0	762	16
BC020708 Homo sapi	625	100.0	762	17
CQ413516 Sequence	1084	100.0	762	18
AX772818 Sequence	1205	94.6	605	19
AX670655 Sequence	1525	83.8	638	20
AX670643 Sequence	1525	83.3	635	21
I08404 Sequence 1	1525	83.3	635	22
AX670647 Sequence	1525	83.3	635	23
AX670647 Sequence	1525	83.3	635	24
A08111 Synthetic A	321	82.9	632	25
A08106 Synthetic A	321	81.8	623	26
A08107 Synthetic A	321	81.8	623	27
A08112 Synthetic A	321	81.8	623	28
A08108 Synthetic A	321	81.5	621	29
A08110 Synthetic A	321	81.5	621	30
A08105 Synthetic A	321	80.6	614	31
A08109 Synthetic A	321	80.6	614	32
X04502 Human SLPI	2657	71.8	547	33
I01501 Sequence 2	545	71.5	545	34
AL035660 Human DNA	63796	70.5	537	35
M57446 Porcine ant	600	66.7	508	36
AF178426 Rattus no	490	63.3	482	37
AF151982 Rattus no	667	61.8	471	38
AF21377 Rattus no	680	61.8	471	39
AX642233 Sequence	396	60.8	463	40
AX642236 Sequence	396	60.8	463	41
AX577885 Sequence	409	60.8	463	42
U88093 Mus musculu	671	60.8	463	43
U94341 Mus musculu	682	60.8	463	44
BC28509 Mus muscu	894	60.8	463	45
U73004 Mus musculu	1123	60.8	463	46
AR270461 Sequence	325	60.1	458	47
AR067991 Sequence	194	45.7	348	48
AY346135 Ovis arie	2737	41.5	316	49
AC094865 Rattus no	2	39.6	302	50
AC112730 Rattus no	2	39.6	302	51
AF205374 Mus muscu	10	37.4	285	52
CQ395755 Sequence	313	37.2	283	53
CQ402085 Sequence	313	37.2	283	54
AF002719 Mus muscu	2435	36.4	277	55
AL590429 Mouse DNA	2	36.4	277	56
AC132741 Rattus no	2	36.4	265	57
AX334505 Sequence	411	34.6	264	58
AX335289 Sequence	411	34.6	264	59
AX335639 Sequence	411	34.6	264	60
M31216 Porcine ute	222	34.3	261	61
CQ408469 Sequence	188	31.9	243	62
BD264991 Compositi	292	29.4	224	63
AR238394 Sequence	292	29.4	224	64
AX366610 Sequence	292	29.4	224	65
BV163497 RPAMSEQO	603	27.1	206	66
BV095123 RPAMSEQO	11	27.1	206	67
AJ005356 Macropus	724	25.9	197	68
AY563621 Xenopus 1	857	25.1	191	69
AY038181 Homo sapi	963	24.6	187	70
BC039173 Homo sapi	1094	24.6	187	71
AY358822 Homo sapi	999	24.3	185	72
BC019734 Mus muscu	1043	24.0	183	73
AF275314 Trichosur	743	23.9	182	74
AF48306 Homo sapi	999	23.6	180	75
X78981 T.trichlura	1486	23.6	180	76
AB076019 Triboledo	1805	23.6	180	77

78 172 22.6 897 9 HS447F331 AL591713 Novel hum
79 171 22.4 2812 3 AF036161 AF036161 Trichuris
80 165.5 21.7 374 6 AX716767 AX716767 Sequence
81 165.5 21.7 375 9 CR456977 CR456977 Homo sapi
82 165.5 21.7 390 6 AX716758 AX716758 Sequence
83 165.5 21.7 486 6 AX716765 AX716765 Sequence
84 165.5 21.7 486 9 AY212888 AY212888 Homo sapi
85 165.5 21.7 500 6 AX588473 AX588473 Sequence
86 165.5 21.7 515 6 AX887924 AX887924 Sequence
87 165.5 21.7 515 6 BD027534 BD027534 Sequence
88 165.5 21.7 566 9 BC046106 BC046106 Homo sapi
89 165.5 21.7 567 6 CQ727374 CQ727374 Sequence
90 165.5 21.7 626 9 BC039816 BC039816 Homo sapi
91 165.5 21.7 634 6 BD203758 BD203758 Human nuc
92 165.5 21.7 634 6 BD222208 BD222208 Human nuc
93 165.5 21.7 634 6 AX014329 AX014329 Sequence
94 165.5 21.7 634 6 AX014913 AX014913 Sequence
95 165.5 21.7 643 6 AX588136 AX588136 Sequence
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100 164.5 21.6 577 6 AX588137 AX588137 Sequence

ALIGNMENTS

RESULT 1
AX302535 AX302535 399 bp DNA linear PAT 30-NOV-2001
LOCUS Sequence 53 from Patent WO0175177.
DEFINITION AX302535
ACCESSION AX302535
VERSION AX302535.1 GI:17383077
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Morin, P.J., Sherman-Baust, C.A., Pizer, E.S. and Hough, C.D.
TITLE Tumor markers in ovarian cancer
JOURNAL Patent: WO 01/5177-A 53 11-OCT-2001;
THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)

FEATURES
source
1. .399
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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ORIGIN

Alignment Scores:
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Score: 762.00 Matches: 132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-613-105-2 (1-132) x AX302535 (1-399)

QY 1 MetLysSerSerGlyLeuPheProPheLeuValLeuLeuAlaLeuGlyThrLeuAlaPro 20
Db 1 ATGAAGTCCAGCGGCTCTTCCCTTCTGTTGCTGCTGGAACTCTGGACCT 60
QY 21 TrpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProProLysLysSer 40
Db 61 TGGGCTGTGGAGGCTCTGGAAGTCTTCAAAGCTGGAGTCTGCTCTCTAAGAAATCT 120
QY 41 AlaGlnCysLeuArgTrpLysLysProGluCysGlnSerAspTrpGlnCysProGlyLys 60
Db 121 GCCCAGTGCCTTAGATACAGAAGACCTGAGTGCAGAGTACTGGCAGTCTCCAGGGAAG 180
QY 61 LysArgCysCysProAspThrCysGlyIleLysCysLeuAspProValAspThrProAsn 80

Db 181 AAGAGATGTTGCTGACACTTGTGGCATCAAAATGCTGGATCCTGTTGACACCCCAAC 240
QY 81 ProThrArgArgLysProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAen 100
Db 241 CCAACAGGAGGAGGAGCTGGGAGTGGCCAGTGACTTATGGCCAATGTTTGATGCTTAAC 300
QY 101 ProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGly 120
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QY 121 MetCysGlyLysSerCysValSerProValLysAla 132
Db 361 ATGTGTGGGAAATCTCGCTTTCCCTGTGAAAGCT 396

RESULT 2

AF114471 AF114471 399 bp mRNA linear PRI 30-MAY-2002
LOCUS Homo sapiens secretory leukocyte proteinase inhibitor precursor,
DEFINITION mRNA, complete cds.
ACCESSION AF114471
VERSION AF114471.1 GI:4378758
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 399)
AUTHORS Si-Tahar, M., Merlin, D., Sitaraman, S. and Madara, J.L.
TITLE Constitutive and regulated secretion of secretory leukocyte
proteinase inhibitor by human intestinal epithelial cells
JOURNAL Gastroenterology 118 (6), 1061-1071 (2000)
MEDLINE 20295039
PUBMED 10833481

REFERENCE 2 (bases 1 to 399)
AUTHORS Si-Tahar, M., Merlin, D., Sitaraman, S. and Madara, J.L.
TITLE Direct Submission
JOURNAL Submitted (16-DEC-1998) Department of Pathology and Clinical
Medicine, Emory University, 1639 Pierce Drive, Atlanta, GA 30322,
USA
FEATURES
source
1. .399
Location/Qualifiers
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/mol_type="mRNA"
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/chromosome="20"
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ORIGIN

Alignment Scores:
Pred. No.: 3 18e-49 Length: 399
Score: 762.00 Matches: 132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-613-105-2 (1-132) x AF114471 (1-399)

QY 1 MetLysSerSerGlyLeuPheProPheLeuValLeuLeuAlaLeuGlyThrLeuAlaPro 20

QY 101 ProProAenPheCysGluMetAseGlyGlnCysLysArgAsePLeuLysCysCysMetGly 120
 |||||
 Db 359 CCCCCCAATTTCTGTGAGATGGATGGCCAGTGAAGCGTGACTTGAAGTGTTCATGGGC 418
 |||||

QY 121 MetCysGlyLysSerCysValSerProValLysAla 132
 |||||
 Db 419 ATGTGTGGGAATCTCGCTTTCCCTGTGAAAGCT 454
 |||||

RESULT 5
 AX069252
 LOCUS AX069252
 DEFINITION Sequence 1 from Patent WO0101998.
 ACCESSION AX069252
 VERSION AX069252.1 GI:12579133
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Neilson,L. and Li,Z.
 TITLE Treatment of endometriosis with antileukoprotease
 JOURNAL Patent: WO 0101998-A 1 11-JAN-2001;
 Reprogen, Inc. (US)
 FEATURES
 Location/Qualifiers
 source
 1..565
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 59..457
 /notes="unnamed protein product"
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ORIGIN
 Alignment Scores:
 Pred. No.: 4.52e-49 Length: 565
 Score: 762.00 Matches: 132
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-613-105-2 (1-132) x AX069252 (1-565)

QY 1 MetLysSerSerGlyLeuPheProPheLeuValLeuAlaLeuGlyThrLeuAlaPro 20
 |||||
 Db 59 ATGAAGTCCAGCGGCCTCTCCCTTCCTGTGCTGCTTCCCTTAGGAATCTGGCACCT 118
 |||||

QY 21 TrpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProProLysLysSer 40
 |||||
 Db 119 TGGGCTGTGGAGGCTCTGGAAAGTCCTTCAAAGCTGGAGTCTGCTCTCTCTAAGAAATCT 178
 |||||

QY 41 AlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAsePTrpGlnCysProGlyLys 60
 |||||
 Db 179 GCCCAGTGCCTTAGATACAAAGAAACCTCGAGTGCAGAGTGAAGTCTCCAGGGAAG 238
 |||||

QY 61 LysArgCysCysProAsePThrCysGlyLysLysCysLeuAsePProValAsePThrProAse 80
 |||||
 Db 239 AAGAGATGTTGTCTGACACTGTGTGGCATCAATATGCTGTGATCTCTGTGACACCCCAAC 298
 |||||

QY 81 ProThrArgArgLysProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAse 100
 |||||
 Db 299 CCAACAGGAGGAGAGCTCGGGAAGTGCAGTGAATATGACCAATGTTGATGCTTAAC 358
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QY 101 ProProAenPheCysGluMetAseGlyGlnCysLysArgAsePLeuLysCysCysMetGly 120
 |||||
 Db 359 CCCCCCAATTTCTGTGAGATGGATGGCCAGTGAAGCGTGACTTGAAGTGTTCATGGGC 418
 |||||

QY 121 MetCysGlyLysSerCysValSerProValLysAla 132
 |||||
 Db 419 ATGTGTGGGAATCTCGCTTTCCCTGTGAAAGCT 454
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RESULT 6
 HSSLIPR
 LOCUS Human SLPI mRNA fragment for secretory leucocyte protease
 DEFINITION inhibitor.
 ACCESSION X04503.1 GI:36490
 VERSION X04503.1
 KEYWORDS elastase inhibitor; protease inhibitor; secretory leucocyte
 protease inhibitor; trypsin inhibitor.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 573)
 AUTHORS Stetler,G., Brewer,M.T. and Thompson,R.C.
 TITLE Isolation and sequence of a human gene encoding a potent inhibitor
 of leukocyte proteases
 JOURNAL Nucleic Acids Res. 14 (20), 7883-7896 (1986)
 MEDLINE 87040761
 PUBMED 3640338
 COMMENT Data kindly reviewed (15-SEP-1987) by Stetler G.
 FEATURES
 Location/Qualifiers
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 1..573
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="parotid gland"
 1..399
 /notes="unnamed protein product; SLPI-precursor"
 /codon_start=1
 /protein_id="CAA28188.1"
 /db_xref="GI:36491"
 /db_xref="GOA:P03973"
 /db_xref="Swiss-Prot:P03973"
 /translation="MKSSGLFPFLVLLALGTLAPWAVEGSGKSFKAGVCPPKSAOCL
 RYKPECQSDWQCPGKKRCCPDTCGKICLDPDVTNPTRPKGKCPVTYGGCLMLNPP
 NFECDGQCKRDLKCCMGCKSCVSPVKA"

sig_peptide
 1..75
 /note="signal peptide (AA -25 to -1)"
 76..396
 /product="mature SLPI (AA 1-107)"
 546..552
 /note="put. polyA signal"
 573
 /note="polyA site"

ORIGIN
 Alignment Scores:
 Pred. No.: 4.59e-49 Length: 573
 Score: 762.00 Matches: 132
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-10-613-105-2 (1-132) x HSSLIPR (1-573)

QY 1 MetLysSerSerGlyLeuPheProPheLeuValLeuAlaLeuGlyThrLeuAlaPro 20
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 Db 1 ATGAAGTCCAGCGGCCTCTTCCCTTCCTGTGCTGCTTGGCTTGGGAATCTGGCACCT 60
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QY 21 TrpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProProLysLysSer 40
 |||||
 Db 61 TGGGCTGTGGAGGCTCTGGAAAGTCCTTCAAAGCTGGAGTCTGCTCTCTAAGAAATCT 120
 |||||

QY 41 AlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAsePTrpGlnCysProGlyLys 60
 |||||
 Db 121 GCCCAGTGCCTTAGATACAAAGAAACCTGAGTGCAGAGTGAAGTGTTCAGGGAAG 180
 |||||

Qy 61 LysArgCysProAspThrCysGlyLeuValLeuAlaLeuGlyThrLeuAlaPro 80
Db 181 AAGAGATGTTGCTGACACTTGTGGCATCAAAATGCTGGATCTGTGTGACACCCCAAC 240
Qy 81 ProThrArgArgLysProGlyLysCysProValThrTyrgLysGlnCysLeuMetLeuAsn 100
Db 241 CCAACAGGAGGAGGCTGGAGAGTGGCCAGTGCCTATGCGCAATGTTTGTGCTTAAC 300
Qy 101 ProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGly 120
Db 301 CCCCCCAATTTCTGTGAGATGGATGGCCAGTGAAGCGTGACITGAAGTGTTCATGGGC 360
Qy 121 MetCysGlyLysSerCysValSerProValLysAla 132
Db 361 ATGTGTGGGAATCCTCGCTTCCCTGTGAAAGCT 396

RESULT 7
CQ727371
LOCUS CQ727371 594 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 13305 from Patent WO02068579.
ACCESSION CQ727371
VERSION CQ727371.1 GI:42293168
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM

REFERENCE 1
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof
JOURNAL Patent: WO 02068579-A 13305 06-SEP-2002;
PE Corporation (NY) (US)
FEATURES
source Location/Qualifiers
1..594
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 4,76e-49 Length: 594
Score: 762.00 Matches: 132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-613-105-2 (1-132) x CQ727371 (1-594)

Qy 1 MetLysSerSerGlyLeuPheProPheLeuValLeuAlaLeuGlyThrLeuAlaPro 20
Db 19 ATGAAGTCCAGCGGCTCTTCCCTTCTGGTGTCTGCTGGCAACTCTGGCACCT 78
Qy 21 TrpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProProLysLysSer 40
Db 79 TGGGCTGTGGAAGGCTCTGGAAGTCTTCAAAGCTGGAGTCTGCTCTCTAAGAAATCT 138
Qy 41 AlaGlnCysLeuArgTyrgLysLysProGluCysGlnSerAspTrpGlnCysProGlyLys 60
Db 139 GCCCAGTGCCTTAGATACAAAGAAACCTGAGTGCAGAGTGACTGGCAGTGTCCAGGGAAG 198
Qy 61 LysArgCysCysProAspThrCysGlyLysLysCysGlyLysCysLeuAspProValAspThrProAsn 80
Db 199 AAGAGATGTTGCTGACACTTGTGGCATCAAAATGCTGGATCTGTTGACACCCCAAC 258
Qy 81 ProThrArgArgLysProGlyLysCysProValThrTyrgLysGlnCysLeuMetLeuAsn 100
Db 259 CCAACAGGAGGAGGCTGGAGAGTGGCAAGTGCCTGAGTGTGCTCTCTAAGAAATCT 318
Qy 101 ProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGly 120
Db 319 CCCCCCAATTTCTGTGAGATGGATGGCCAGTGAAGCGTGACTTGAAGTGTTCATGGGC 378

RESULT 9
AX328399
LOCUS AX328399 594 bp DNA linear PAT 07-JAN-2002
DEFINITION Sequence 1 from Patent WO0190421.
ACCESSION AX328399
VERSION AX328399.1 GI:18098360
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM

Db 319 CCCCCCAATTTCTGTGAGATGGATGGCCAGTGAAGCGTGACTTGAAGTGTTCATGGGC 378
Qy 121 MetCysGlyLysSerCysValSerProValLysAla 132
Db 379 ATGTGTGGGAATCCTCGCTTCCCTGTGAAAGCT 414

RESULT 8
AR270708
LOCUS AR270708 594 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 1271 from patent US 6500938.
ACCESSION AR270708
VERSION AR270708.1 GI:29701942
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 594)
AUTHORS Au-Young, J. and Seilhamer, J.J.
TITLE Composition for the detection of signaling pathway gene expression
JOURNAL Patent: US 6500938-A 1271 31-DEC-2002;
FEATURES
Location/Qualifiers
source 1..594
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 4,76e-49 Length: 594
Score: 762.00 Matches: 132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-613-105-2 (1-132) x AR270708 (1-594)

Qy 1 MetLysSerSerGlyLeuPheProPheLeuValLeuAlaLeuGlyThrLeuAlaPro 20
Db 19 ATGAAGTCCAGCGGCTCTTCCCTTCTGGTGTCTGCTGGCAACTCTGGCACCT 78
Qy 21 TrpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProProLysLysSer 40
Db 79 TGGGCTGTGGAAGGCTCTGGAAGTCTTCAAAGCTGGAGTCTGCTCTCTAAGAAATCT 138
Qy 41 AlaGlnCysLeuArgTyrgLysLysProGluCysGlnSerAspTrpGlnCysProGlyLys 60
Db 139 GCCCAGTGCCTTAGATACAAAGAAACCTGAGTGCAGAGTGACTGGCAGTGTCCAGGGAAG 198
Qy 61 LysArgCysCysProAspThrCysGlyLysLysCysGlyLysCysLeuAspProValAspThrProAsn 80
Db 199 AAGAGATGTTGCTGACACTTGTGGCATCAAAATGCTGGATCTGTTGACACCCCAAC 258
Qy 81 ProThrArgArgLysProGlyLysCysProValThrTyrgLysGlnCysLeuMetLeuAsn 100
Db 259 CCAACAGGAGGAGGCTGGAGAGTGGCAAGTGCCTGAGTGTGCTCTCTAAGAAATCT 318
Qy 101 ProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGly 120
Db 319 CCCCCCAATTTCTGTGAGATGGATGGCCAGTGAAGCGTGACTTGAAGTGTTCATGGGC 378

RESULT 10
AX328399
LOCUS AX328399 594 bp DNA linear PAT 07-JAN-2002
DEFINITION Sequence 1 from Patent WO0190421.
ACCESSION AX328399
VERSION AX328399.1 GI:18098360
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

Rastelli, L. and Smithson, G.

Method of detecting inflammatory lung disorders

Patent: WO 0190421-A 1 29-NOV-2001;

Curagen Corporation (US)

Location/Qualifiers

1..594

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Alignment Scores: 4.76e-49 Length: 594

Pred. No.: 762.00 Matches: 132

Score: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-10-613-105-2 (1-132) x AX328399 (1-594)

QY 1 MetLysSerSerGlyLeuPheProPheLeuValLeuAlaLeuGlyThrLeuAlaPro 20

DB 19 ATGAAGTCCAGCGGCTCTTCCCTTCTCGTGCTGCTTCCCTGGGAACTCTGGCACCT 78

QY 21 TPAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProLysLysSer 40

DB 79 TGGGCTGTGGAGGCTCTGGAAGTCTTCAAGCTGGAGTCTGCTCTCTAAGAAATCT 138

QY 41 AlaGlnCysLeuArgTyrLysProGluCysGlnSerAspTrpGlnCysProGlyLys 60

DB 139 GCCCAGTGGCTTAGATACAAAGAACCTGAGTGCAGAGTGACCTGGCAGGTGCCAGGGAAG 198

QY 61 LysArgCysCysProAspThrCysGlyLysCysLeuAspProValAspThrProAsn 80

DB 199 AAGAGATGTTGCTTGACACTTGGGATCAATGCTGATCTGTTGACACCCCAAC 258

QY 81 ProThrArgArgLysProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAsn 100

DB 259 CCACCAAGGAGGAGCGCTGGGAAGTCCAGTACTTATGGCCAATGTTGATGCTTAAAC 318

QY 101 ProProAsnPheCysGluMetAspGlyLysCysLysArgAspLeuLysCysCysMetGly 120

DB 319 CCCCCCAATTTCTGTGAGATGGATGGCCAGTGCAGGTGACCTTGAAGTGTTCATGGGC 378

QY 121 MetCysGlyLysSerCysValSerProValLysAla 132

DB 379 ATGTGTGGGAAATCTGCGTTTCCCTGTGAAGCT 414

RESULT 10

AX334507

LOCUS

Sequence 5016 from Patent WO0194629.

AX334507

ACCESSION

AX334507.1 GI:18125226

VERSION

KEYWORDS

source

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,

Horrigan, S., Soppet, D.R. and Weaver, Z.

Cancer gene determination and therapeutic screening using signature

gene sets

Patent: WO 0194629-A 5016 13-DEC-2001;

Avalon Pharmaceuticals (US)

Location/Qualifiers

1..594

/organism="Homo sapiens"

/db_xref="taxon:9606"

ORIGIN

Alignment Scores: 4.76e-49 Length: 594

Pred. No.: 762.00 Matches: 132

Score: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Alignment Scores: 4.76e-49 Length: 594

Pred. No.: 762.00 Matches: 132

Score: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-10-613-105-2 (1-132) x AX334507 (1-594)

QY 1 MetLysSerSerGlyLeuPheProPheLeuValLeuAlaLeuGlyThrLeuAlaPro 20

DB 19 ATGAAGTCCAGCGGCTCTTCCCTTCTCGTGCTGCTTCCCTGGGAACTCTGGCACCT 78

QY 21 TPAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProLysLysSer 40

DB 79 TGGGCTGTGGAGGCTCTGGAAGTCTTCAAGCTGGAGTCTGCTCTCTAAGAAATCT 138

QY 41 AlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAspTrpGlnCysProGlyLys 60

DB 139 GCCCAGTGGCTTAGATACAAAGAACCTGAGTGCAGAGTGACCTGGCAGGTGCCAGGGAAG 198

QY 61 LysArgCysCysProAspThrCysGlyLysCysLeuAspProValAspThrProAsn 80

DB 199 AAGAGATGTTGCTTGACACTTGTGGCATCAATGCTGATCTGTTGACACCCCAAC 258

QY 81 ProThrArgArgLysProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAsn 100

DB 259 CCACCAAGGAGGAGCGCTGGGAAGTCCAGTACTTATGGCCAATGTTGATGCTTAAAC 318

QY 101 ProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGly 120

DB 319 CCCCCCAATTTCTGTGAGATGGATGGCCAGTGCAGGTGACCTTGAAGTGTTCATGGGC 378

QY 121 MetCysGlyLysSerCysValSerProValLysAla 132

DB 379 ATGTGTGGGAAATCTGCGTTTCCCTGTGAAGCT 414

RESULT 11

AX335376

LOCUS

Sequence 5985 from Patent WO0194629.

AX335376

ACCESSION

AX335376.1 GI:18126095

VERSION

KEYWORDS

source

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,

Horrigan, S., Soppet, D.R. and Weaver, Z.

Cancer gene determination and therapeutic screening using signature

gene sets

Patent: WO 0194629-A 5985 13-DEC-2001;

Avalon Pharmaceuticals (US)

Location/Qualifiers

1..594

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Alignment Scores: 4.76e-49 Length: 594

Pred. No.: 762.00 Matches: 132

Score: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

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DB: 6 Gaps: 0
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QY 21 TrpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProProLysLysSer 40
Db 79 TGGGCTGTGGAAGGCTCTGGAAGTCTCTCAAGCTGGAGTCTGCTCTCTCAAGAAATCT 138
QY 41 AlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAspTrpGlnCysProGlyLys 60
Db 139 GCCCAGTGCCTTAGATACAAAGAACTGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAG 198
QY 61 LysArgCysCysProAspThrCysGlyLysLysCysGlyLysCysLeuAspProValAspThrProAsn 80
Db 199 AAGAGATGTTGCTGACACTTGTGGCATAAATGCTGGATCTCTGTTGACACCCCAAC 258
QY 81 ProThrArgLysProGlyLysSerPheLysAlaGlyValCysProProLysLysSer 40
Db 79 TGGGCTGTGGAAGGCTCTGGAAGTCTCTCAAGCTGGAGTCTGCTCTCTCAAGAAATCT 138
QY 41 AlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAspTrpGlnCysProGlyLys 60
Db 139 GCCCAGTGCCTTAGATACAAAGAACTGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAG 198
QY 61 LysArgCysCysProAspThrCysGlyLysLysCysGlyLysCysLeuAspProValAspThrProAsn 80
Db 199 AAGAGATGTTGCTGACACTTGTGGCATAAATGCTGGATCTCTGTTGACACCCCAAC 258
QY 81 ProThrArgLysProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAsn 100
Db 259 CCAACAAGGAGGAAGCTTGGGAAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAG 318
QY 101 ProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGly 120
Db 319 CCCCCCAATTTCTGTGAGATGGATGCCAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAG 378
QY 121 MetCysGlyLysSerCysValSerProValLysAla 132
Db 379 ATGTGTGGGAATCTGCGTTTCCCTGTGAAAGCT 414

RESULT 13
AX577960
LOCUS AX577960 594 bp DNA linear PAT 08-JAN-2003
DEFINITION Sequence 82 from Patent WO02081745.
ACCESSION AX577960
VERSION AX577960.1 GI:27647168
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Connolly,T., Roman Roman,S., Baron,R., Call,K., Theilhaber,J.,
Garcia,T., Jackson,A., Bushnell,S.E. and Rawadi,G.
TITLE Genes involved in osteogenesis and methods of use
JOURNAL Patent: WO 02081745-A 82 17-OCT-2002;
Aventis Pharma S.A. (FR)
FEATURES
source 1..594
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 4,76e-49 Length: 594
Score: 762.00 Matches: 132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-613-105-2 (1-132) x AX577960 (1-594)
QY 1 MetLysSerGlyLeuPheProPheLeuValLeuAlaLeuGlyThrLeuAlaPro 20
Db 19 ATGAAGTCCAGCGCCCTCTCCCTTCCTGGTGTCTGCTGGCACTCTGGACCT 78
QY 21 TrpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProProLysLysSer 40
Db 79 TGGGCTGTGGAAGGCTCTGGAAGTCTCTCAAGCTGGAGTCTGCTCTCTCAAGAAATCT 138
QY 41 AlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAspTrpGlnCysProGlyLys 60
Db 139 GCCCAGTGCCTTAGATACAAAGAACTGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAG 198
QY 61 LysArgCysCysProAspThrCysGlyLysLysCysGlyLysCysLeuAspProValAspThrProAsn 80
Db 199 AAGAGATGTTGCTGACACTTGTGGCATAAATGCTGGATCTCTGTTGACACCCCAAC 258
QY 81 ProThrArgLysProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAsn 100
Db 259 CCAACAAGGAGGAAGCTTGGGAAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAG 318
QY 101 ProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGly 120
Db 319 CCCCCCAATTTCTGTGAGATGGATGCCAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAG 378
QY 121 MetCysGlyLysSerCysValSerProValLysAla 132
Db 379 ATGTGTGGGAATCTGCGTTTCCCTGTGAAAGCT 414

RESULT 12
AX577960
LOCUS AX577960 594 bp DNA linear PAT 08-JAN-2003
DEFINITION Sequence 82 from Patent WO02081745.
ACCESSION AX577960
VERSION AX577960.1 GI:27647168
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Connolly,T., Roman Roman,S., Baron,R., Call,K., Theilhaber,J.,
Garcia,T., Jackson,A., Bushnell,S.E. and Rawadi,G.
TITLE Genes involved in osteogenesis and methods of use
JOURNAL Patent: WO 02081745-A 82 17-OCT-2002;
Aventis Pharma S.A. (FR)
FEATURES
source 1..594
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 4,76e-49 Length: 594
Score: 762.00 Matches: 132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-613-105-2 (1-132) x AX780010 (1-594)
QY 1 MetLysSerGlyLeuPheProPheLeuValLeuAlaLeuGlyThrLeuAlaPro 20
Db 19 ATGAAGTCCAGCGCCCTCTCCCTTCCTGGTGTCTGCTGGCACTCTGGACCT 78
QY 21 TrpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProProLysLysSer 40
Db 79 TGGGCTGTGGAAGGCTCTGGAAGTCTCTCAAGCTGGAGTCTGCTCTCTCAAGAAATCT 138
QY 41 AlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAspTrpGlnCysProGlyLys 60
Db 139 GCCCAGTGCCTTAGATACAAAGAACTGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAG 198
QY 61 LysArgCysCysProAspThrCysGlyLysLysCysGlyLysCysLeuAspProValAspThrProAsn 80
Db 199 AAGAGATGTTGCTGACACTTGTGGCATAAATGCTGGATCTCTGTTGACACCCCAAC 258

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QY      1  MetLysSerSerGlyLeuPheProPheLeuValLeuLeuAlaLeuGlyThrLeuAlaPro 20
DB      14  ATGAAGTCCAGCGGCTCTTCCCTTCTGGTCTGCTTGGCACTCTGGCACCT 73

QY      21  TrpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProProLysLysSer 40
DB      74  TGGGCTGTGGAGGCTCTGGAAAGTCTTCAAGAGCTGGAGTCTGCTCTCTAAGAAATCT 133

QY      41  AlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAspTrpGlnCysProGlyLys 60
DB      134  GCCAGTGCCTTAGATACAGAAGAACTGAGTGCAGAGTGACTGGCAGTGTCCAGGGAAG 193

QY      61  LysArgCysCysProAspThrCysGlyLysCysLeuAspProValAspThrProAsn 80
DB      194  AAGAGATGTTGCTGCACACTTGTGGCATCAAAATGCTGGATCTGTTGTGACACCCCAAC 253

QY      81  ProThrArgArgLysProGlyLysCysProValThrTyrGlnCysLeuMetLeuAsn 100
DB      254  CCAACAAGGAGGAGGAGCTGGGAAGTCCCAAGTGCATCTATGCCCCTGTTGATGCTTAAC 313

QY      101  ProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGly 120
DB      314  CCCCCCAATTTCTGTGAGATGGATGCCAGTGCACGTCGACTTGAAGTGTTCATGGGC 373

QY      121  MetCysGlyLysSerCysValSerProValLysAla 132
DB      374  ATGTGTGGGAAATCTCGCGTTTCCCTGTGAAAGCT 409

RESULT 16
AX014898
LOCUS      AX014898
DEFINITION Sequence 97 from Patent WO9953040.
ACCESSION AX014898
VERSION    AX014898.1 GI:10041165
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1  Schmitt,A., Specht,T., Dahl,B., Hinzmann,B., Rosenthal,A. and
AUTHORS    Pilarsky,C.
TITLE      Human nucleic acid sequences from ovarian tumour tissue
JOURNAL    Patent: WO 9953040-A 97 21-OCT-1999;
            SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN
            BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GES FUER GENOMFORSCHUN
            (DE); PILARSKY CHRISTIAN (DE)
FEATURES   Location/Qualifiers
            source
              1. .599
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.:      4.8e-49      Length:      599
Score:          762.00      Matches:    132
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             6           Gaps:        0

US-10-613-105-2 (1-132) x AX014898 (1-599)

QY      1  MetLysSerSerGlyLeuPheProPheLeuValLeuLeuAlaLeuGlyThrLeuAlaPro 20
DB      14  ATGAAGTCCAGCGGCTCTTCCCTTCTGGTCTGCTTGGCACTCTGGCACCT 73

QY      21  TrpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProProLysLysSer 40
DB      74  TGGGCTGTGGAGGCTCTGGAAAGTCTTCAAGAGCTGGAGTCTGCTCTCTAAGAAATCT 133

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QY      41  AlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAspTrpGlnCysProGlyLys 60
DB      134  GCCCAGTGCCTTAGATACAGAAGAACTGAGTGCAGAGTGACTGGCAGTGTCCAGGGAAG 193

QY      61  LysArgCysCysProAspThrCysGlyLysCysLeuAspProValAspThrProAsn 80
DB      194  AAGAGATGTTGCTGCACACTTGTGGCATCAAAATGCTGGATCTGTTGTGACACCCCAAC 253

QY      81  ProThrArgArgLysProGlyLysCysProValThrTyrGlnCysLeuMetLeuAsn 100
DB      254  CCAACAAGGAGGAGGAGCTGGGAAGTCCCAAGTGCATCTATGCCCCTGTTGATGCTTAAC 313

QY      101  ProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGly 120
DB      314  CCCCCCAATTTCTGTGAGATGGATGCCAGTGCACGTCGACTTGAAGTGTTCATGGGC 373

QY      121  MetCysGlyLysSerCysValSerProValLysAla 132
DB      374  ATGTGTGGGAAATCTCGCGTTTCCCTGTGAAAGCT 409

RESULT 17
BC020708
LOCUS      BC020708
DEFINITION Homo sapiens secretory leukocyte protease inhibitor
            (antileukoprotease), mRNA (cDNA clone MGC:22479 IMAGE:4733996),
            complete cds.
ACCESSION BC020708
VERSION    BC020708.1 GI:18088404
KEYWORDS   MGC.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1  (bases 1 to 625)
AUTHORS    Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Schetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raja,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullaly,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Kettaman,M., Madan,A., Rodriguez,S.,
            Sanchez,A., Whitting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalls,D.E.,
            Scherch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
            Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
            Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
            12477932
            2  (bases 1 to 625)
            Strausberg,R.
            Direct Submission
            Submitted (03-JAN-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
            NIH-MGC Project URL: http://mgc.nci.nih.gov
            Contact: MGC help desk
            Email: cgapsb-r@mail.nih.gov
            Tissue Procurement: CLONTECH
            cDNA Library Preparation: CLONTECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA 94305
            Web site: http://www.shgc.stanford.edu
            Contact: (Dickson, Mark) mcd@paxil.stanford.edu

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Bejanin, S. and Tanaka, H.
TITLE Human cDNAs and proteins and uses thereof
JOURNAL Patent: WO 03046180-A 15 05-JUN-2003;
Genset S.A. (FR)

FEATURES
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1. .605
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1. .121
22. .363
/notes="unnamed protein product"
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3'UTR 361. .605
polyA_signal 565. .570
polyA_site 590. .605

ORIGIN
Alignment Scores:
Pred. No.: 6 62e-46 Length: 605
Score: 720.50 Matches: 129
Percent Similarity: 97.73% Conservative: 0
Best Local Similarity: 97.73% Mismatches: 2
Query Match: 94.55% Indels: 2
DB: 6 Gaps: 1

US-10-613-105-2 (1-132) x AX772818 (1-605)

QY 1 MetLysSerSerGlyLeuPheProPheLeuValLeuAlaLeuGlyThrLeuAlaPro 20
DB 22 ATCAAGTCCAGCGGCTCTTCCCTTCCTGCTGCTGCTGCCCTGGGAACCTCTGGCACCT 81
QY 21 TrpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProProLysLysSer 40
DB 82 TGGGCTGTGGAGGCTCTGGAAGTCTCTCAAGCTGGAGTCTGCTCTCTAAGAAATCT 141
QY 41 AlaGlnCysLeuArgTrpLysLysProGluCysGlnSerAspTrpGlnCysProGlyLys 60
DB 142 GCCAGTGCCTTAGATACAGAAACCTGAGTGCAGAGTACTGGCAGTGTCCAGGGAAG 201
QY 61 LysArgCysCysProAspThrCysGlyIleLysCysLeuAspProValAspThrProAsn 80
DB 202 AAGAGATGTGCTCGACACTTGTGGCATCAATGCTGGATCCTGTGTGACACCCCAAC 261
QY 81 ProThrArgArgLysProGlyLysCysProValThrTrpGlyGlnCysLeuMetLeuAsn 100
DB 262 CCAACAAGGAGGAAGCTGGGAAGTGGCCAGTACTTATGGCAATGTTTGTATGCTTAAC 321
QY 101 ProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGly 120
DB 322 CCCCCCAATTCGTGAGATGGATGGCCAGTGGCT-TAC---TTGAAGTGTTCATGGGC 377
QY 121 MetCysGlyLysSerCysValSerProValLysAla 132
DB 378 ATGTGTGGGAATCCTGCGTTTCCCTGTGAAGCT 413

RESULT 20
AX670655
LOCUS AX670655
DEFINITION Sequence 15 from Patent WO0250287.
ACCESSION AX670655
VERSION AX670655.1 GI:29292050
KEYWORDS
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Barr, P.J., Gibson, H.L. and Pemberton, P.
TITLE Multifunctional protease inhibitors and their use in treatment of disease
JOURNAL Patent: WO 0250287-A 15 27-JUN-2002;
Arriva Pharmaceuticals, Inc. (US)

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1. .1525
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ORIGIN
Alignment Scores:
Pred. No.: 2 64e-39 Length: 1525
Score: 638.50 Matches: 112
Percent Similarity: 87.97% Conservative: 5
Best Local Similarity: 84.21% Mismatches: 9
Query Match: 83.79% Indels: 7
DB: 6 Gaps: 1

US-10-613-105-2 (1-132) x AX670655 (1-1525)

QY 7 PheProPheLeuValLeu-----LeuAlaLeuGlyThrLeuAla 19
DB 1119 TTCGTTTTTCTGATGATCGAGCAGAACACTAAAGGCCATTTTATGGTAAAGTTGTC 1178
QY 20 ProTrpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProProLysLys 39
DB 1179 AACCCAACTCAGAAGATGTCGGAAGTCTTTCAGGCGCGTGTTCACCAAGAAAG 1238
QY 40 SerAlaGlnCysLeuArgTrpLysLysProGluCysGlnSerAspTrpGlnCysProGly 59
DB 1239 TCCGCTCAATGTTTGAGATACAGAGCCAGCAATGTCATCCAGCTGGCAATGTCAGGT 1298
QY 60 LysLysArgCysCysProAspThrCysGlyIleLysCysLeuAspProValAspThrPro 79
DB 1299 AAGAAGAGATGTTGTCAGACACTTGTGGTATCATCAAGTGTCTAGACCCAGTTGACACCCA 1358
QY 80 AsnProThrArgArgLysProGlyLysCysProValThrTrpGlyGlnCysLeuMetLeu 99
DB 1359 AACCCAACTAGAGAAAGCCAGGTAAGTGTCCAGTTACTTACGTCCTCAATGTTGATGTTG 1418
QY 100 AsnProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCysMet 119
DB 1419 AACCCCAAACTCTGTGAATGGACGGTCAATGTAAAGAGAGACTTGAAGTGTGTATG 1478
QY 120 GlyMetCysGlyLysSerCysValSerProValLysAla 132
DB 1479 GGTATGTGTGTAAGTCTGTGTTTCCCGCAGTCAAGGCC 1517

RESULT 21
AX670643
LOCUS AX670643
DEFINITION Sequence 3 from Patent WO0250287.
ACCESSION AX670643
VERSION AX670643.1 GI:29292045
KEYWORDS
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Barr, P.J., Gibson, H.L. and Pemberton, P.
TITLE Multifunctional protease inhibitors and their use in treatment of disease
JOURNAL Patent: WO 0250287-A 3 27-JUN-2002;
Arriva Pharmaceuticals, Inc. (US)

FEATURES
source
1. .321


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Db      252  GAAATGACGGTCAATGTAAGAGAGACTTGAAGTGTGTATGGTATGTGTGTAAGTCC 311
QY      126  CysValSerProVallysala 132
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Db      312  TGTGTTTCCCAAGTCAAGGCC 332

RESULT 24
A08111
LOCUS      Synthetic ALP-gene 242.          321 bp      DNA      linear      PAT 28-JUL-1993
DEFINITION
ACCESSION  A08111
VERSION    A08111.1  GI:413358
KEYWORDS   .
SOURCE     .
ORGANISM   .
            synthetic construct
            artificial construct
            sequences.
REFERENCE  1 (bases 1 to 321)
AUTHORS   Heinzl-Wieland, R., Ammann, J., Steffens, G.J. and Flohe, L.
TITLE     Serine protease inhibitor proteins, medicaments containing them,
          DNA sequences coding for these proteins and methods for producing
          these proteins, medicaments and DNA sequences
          Patent: EP 0373335-A 33 20-JUN-1990;
          Gruenenthal GmbH
JOURNAL
FEATURES   Location/Qualifiers
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              1..321
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                SPVKA"

ORIGIN
Alignment Scores:      1.69e-39      Length:      321
Pred. No.:      632.00      Matches:      106
Score:      100.00%      Conservative:      1
Percent Similarity:      99.07%      Mismatches:      0
Best Local Similarity:      82.94%      Indels:      0
Query Match:      6      Gaps:      0
DB:
US-10-613-105-2 (1-132) x A08111 (1-321)

QY      26  SerGlyLysSerPhelysAlaGlyValCysProProLysLysSerAlaGlnCysLeuArg 45
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Db      1  AGCGGTAAGTCTTTCAAGCCGCGTCTGTCTCTCTTAAGAAATCTGCTCAGTGCCTCGGT 60

QY      46  TyrLysLysProGluCysGlnSerAspTTPGlnCysProGlyLysLysArgCysCysPro 65
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Db      61  TACAAGAAACCCGAGTGCCAGTCTGACTGGCAGTGTCTGTTGAAGAAGCGTTGTTGCTCT 120

QY      66  AspThrCysGlyLysLysCysGlnSerAspTTPGlnCysProGlyLysLysArgCysCysPro 65
      |||||
Db      61  TACAAGAAACCCGAGTGCCAGTCTGACTGGCAGTGTCTGTTGAAGAAGCGTTGTTGCTCT 120

QY      66  AspThrCysGlyLysLysCysGlnSerAspTTPGlnCysProGlyLysLysArgCysCysPro 85
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Db      121  GACACTTGTGTATCAAAATCGCTGGATCCGTTGACACCCGAAACCGACGCGTCTGCTAA 180

QY      86  ProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAsnProProAsnPheCys 105
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Db      121  GACACTTGTGTATCAAAATCGCTGGATCCGTTGACACCCGAAACCGACGCGTCTGCTAA 180

QY      86  ProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAsnProProAsnPheCys 105
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Db      181  CCCGGGAAGTCCCGGTTACCTACGGTCAGTGTCTGCTGAACCCGCTAACTTCTGCT 240

QY      106  GluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGlyMetCysGlyLysSer 125
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QY      126  CysValSerProVallysala 132
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Db      301  TCGTTAGCCCGGTTAAGGCT 321

RESULT 25
A08106
LOCUS      Synthetic ALP-gene 240.          321 bp      DNA      linear      PAT 28-JUL-1993
DEFINITION
ACCESSION  A08106
VERSION    A08106.1  GI:413348
KEYWORDS   .
SOURCE     .
ORGANISM   .
            synthetic construct
            artificial construct
            sequences.
REFERENCE  1 (bases 1 to 321)
AUTHORS   Heinzl-Wieland, R., Ammann, J., Steffens, G.J. and Flohe, L.
TITLE     Serine protease inhibitor proteins, medicaments containing them,
          DNA sequences coding for these proteins and methods for producing
          these proteins, medicaments and DNA sequences
          Patent: EP 0373335-A 28 20-JUN-1990;
          Gruenenthal GmbH
JOURNAL
FEATURES   Location/Qualifiers
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                SPVKA"

ORIGIN
Alignment Scores:      8.1e-39      Length:      321
Pred. No.:      623.00      Matches:      105
Score:      99.07%      Conservative:      1
Percent Similarity:      98.13%      Mismatches:      0
Best Local Similarity:      81.76%      Indels:      0
Query Match:      6      Gaps:      0
DB:
US-10-613-105-2 (1-132) x A08106 (1-321)

QY      26  SerGlyLysSerPhelysAlaGlyValCysProProLysLysSerAlaGlnCysLeuArg 45
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Db      1  AGCGGTAAGTCTTTCAAGCCGCGTCTGTCTCTCTTAAGAAATCTGCTCAGTGCCTCGGT 60

QY      46  TyrLysLysProGluCysGlnSerAspTTPGlnCysProGlyLysLysArgCysCysPro 65
      |||||
Db      61  TACAAGAAACCCGAGTGCCAGTCTGACTGGCAGTGTCTGTTGAAGAAGCGTTGTTGCTCT 120

QY      66  AspThrCysGlyLysLysCysGlnSerAspTTPGlnCysProGlyLysLysArgCysCysPro 85
      |||||
Db      121  GACACTTGTGTATCAAAATCGCTGGATCCGTTGACACCCGAAACCGACGCGTCTGCTAA 180

QY      86  ProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAsnProProAsnPheCys 105
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Db      181  CCCGGGAAGTCCCGGTTACCTACGGTCAGTGTCTGCTGAACCCGCTAACTTCTGCT 240

QY      106  GluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGlyMetCysGlyLysSer 125
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Db      241  GAGATGGATGGCCAGTGCAACGAGATCTGAATGCTGATGGTATGTGCGGTAAAGC 300

QY      126  CysValSerProVallysala 132
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Db      301  TCGTTAGCCCGGTTAAGGCT 321

RESULT 26
A08107

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LOCUS A08107 321 bp DNA linear PAT 28-JUL-1993
DEFINITION Synthetic ALP-gene 231.
ACCESSION A08107
VERSION A08107.1 GI:413350
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1 (bases 1 to 321)
Heinzel-Wieland,R., Ammann,J., Steffens,G.J. and Flohe,L.
AUTHORS Serine protease inhibitor proteins, medicaments containing them,
TITLE DNA sequences coding for these proteins and methods for producing
these proteins, medicaments and DNA sequences
JOURNAL Patent: EP 0373335-A 29 20-JUN-1990;
Gruenthal GmbH
FEATURES
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ORIGIN
Alignment Scores: 8.1e-39 Length: 321
Pred. No.: 623.00 Matches: 103
Score: 100.00% Conservative: 4
Percent Similarity: 96.26% Mismatches: 0
Best Local Similarity: 81.76% Indels: 0
Query Match: 6 Gaps: 0
DB: 6
US-10-613-105-2 (1-132) x A08107 (1-321)
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Db 1 ACCGGTAAGTCTTTCAAGCCGCGTCTGCTCTCTTAAGAAATCTGCTCAGTGCCTGCGT 60
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Db 61 TACAAGAAACCCGAGTGCCAGTCTGACTGGCAGTGTCTGGTAAAGAGCGTTGTGTCT 120
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QY 66 AspThrCysGlyLeuLysCysLeuAspProValAspThrProAsnProThrArgArgLys 85
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Db 121 GACACTTGTGGTATCAAAATCGCTGGATCGGTTGACACCCGAAACCCGACGCGTCTGATAA 180
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QY 86 ProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAsnProProAsnPheCys 105
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Db 181 CCCGGAAGTGCCCGGTACCTACGTACGTGCTGCTGCTGAACCCGCTTAACCTCTGTC 240
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QY 106 GluMetAspGlyGlnCysLysArgAspLeuLysCysMetGlyMetCysGlyLysSer 125
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Db 241 GAGCTCGATGGCCAGTGCAAAAGAGATCTGAATGCTGCTGCTGAACCCGCTTAACCTCTGTC 300
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QY 126 CysValSerProValLysAla 132
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Db 301 TCGGTTAGCCCGGTTAAGGCT 321
RESULT 27
A08112
LOCUS A08112 321 bp DNA linear PAT 28-JUL-1993
DEFINITION Synthetic ALP-gene 246.
ACCESSION A08112
VERSION A08112.1 GI:413360

KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1 (bases 1 to 321)
Heinzel-Wieland,R., Ammann,J., Steffens,G.J. and Flohe,L.
AUTHORS Serine protease inhibitor proteins, medicaments containing them,
TITLE DNA sequences coding for these proteins and methods for producing
these proteins, medicaments and DNA sequences
JOURNAL Patent: EP 0373335-A 34 20-JUN-1990;
Gruenthal GmbH
FEATURES
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SPVKA"
ORIGIN
Alignment Scores: 8.1e-39 Length: 321
Pred. No.: 623.00 Matches: 105
Score: 99.07% Conservative: 1
Percent Similarity: 98.13% Mismatches: 1
Best Local Similarity: 81.76% Indels: 0
Query Match: 6 Gaps: 0
DB: 6
US-10-613-105-2 (1-132) x A08112 (1-321)
QY 26 SerGlyLysSerPhelysAlaGlyValCysProProLysLysSerAlaGlnCysLeuArg 45
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Db 1 ACCGGTAAGTCTTTCAAGCCGCGTCTGCTCTCTTAAGAAATCTGCTCAGTGCCTGCGT 60
|||
QY 46 TyrLysLysProGluCysGlnSerAspTTPGlnCysProGlyLysLysArgCysPro 65
|||
Db 61 TACAAGAAACCCGAGTGCCAGTCTGACTGGCAGTGTCTGGTAAAGAGCGTTGTGTCT 120
|||
QY 66 AspThrCysGlyLeuLysCysLeuAspProValAspThrProAsnProThrArgArgLys 85
|||
Db 121 GACACTTGTGGTATCAAAATCGCTGGATCGGTTGACACCCGAAACCCGACGCGTCTGATAA 180
|||
QY 86 ProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAsnProProAsnPheCys 105
|||
Db 181 CCCGGAAGTGCCCGGTACCTACGTACGTGCTGCTGCTGAACCCGCTTAACCTCTGTC 240
|||
QY 106 GluMetAspGlyGlnCysLysArgAspLeuLysCysMetGlyMetCysGlyLysSer 125
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Db 241 GAGATGATGGCCAGTGCAAAAGAGATCTGAATGCTGCTGCTGAACCCGCTTAACCTCTGTC 300
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QY 126 CysValSerProValLysAla 132
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Db 301 TCGGTTAGCCCGGTTAAGGCT 321
RESULT 28
A08108
LOCUS A08108 321 bp DNA linear PAT 28-JUL-1993
DEFINITION Synthetic ALP-gene 232.
ACCESSION A08108
VERSION A08108.1 GI:413352
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1 (bases 1 to 321)
Heinzel-Wieland,R., Ammann,J., Steffens,G.J. and Flohe,L.
AUTHORS Serine protease inhibitor proteins, medicaments containing them,
TITLE DNA sequences coding for these proteins and methods for producing
these proteins, medicaments and DNA sequences
JOURNAL Patent: EP 0373335-A 30 20-JUN-1990;
Gruenthal GmbH
FEATURES Location/Qualifiers
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CDS 1..321
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SPVKA"
ORIGIN
Alignment Scores: 1.15e-38 Length: 321
Pred. No.: 621.00 Matches: 102
Score: 100.00% Conservative: 5
Percent Similarity: 95.33% Mismatches: 0
Best Local Similarity: 81.50% Indels: 0
Query Match: 6 Gaps: 0
DB: 6
US-10-613-105-2 (1-132) x A08108 (1-321)
Qy 26 SerGlyLysSerPheLysAlaGlyValCysProProLysLysSerAlaGlnCysLeuArg 45
Db 1 AGCGGTAAGTCTTTCAAAGCCGGCTGTCTCCTTAAGAAATCTGCTCAGTGCCTGCGT 60
Qy 46 TyrLysLysProGluCysGlnSerAspTTPGlnCysProGlyLysLysArgCysCysPro 65
Db 61 TACAAGNAACCCGAGTGCAGTCTGACTGCGAGTGTCTGTTAAGAACGCTTGTGTCTT 120
Qy 66 AspThrCysGlyLysCysLeuAspProValAspThrProAsnProThrArgArgLys 85
Db 121 GACACTTGTGTATCAATGCCCTGGATCGGTTGACACCCGACCGCGCTCGTAAA 180
Qy 86 ProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAsnProProAsnPheCys 105
Db 181 CCCGGGAAGTGCCTGATCGGTTACCTACGGTCACTGCTGCTGCTGCTGCTGCTGCTG 240
Qy 106 GluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGlyMetCysGlyLysSer 125
Db 241 GAGCTCGATGCCGAGTGCACCAACGAGATCTGAAATGCTGCTGCTGCTGCTGCTGCTG 300
RESULT 29
A08110
LOCUS A08110 321 bp DNA linear PAT 28-JUL-1993
DEFINITION Synthetic ALP-gene 237.
ACCESSION A08110
VERSION A08110.1 GI:413356
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 321)
AUTHORS Heinzel-Wieland,R., Ammann,J., Steffens,G.J. and Flohe,L.
TITLE Serine protease inhibitor proteins, medicaments containing them,
DNA sequences coding for these proteins and methods for producing

these proteins, medicaments and DNA sequences
JOURNAL Patent: EP 0373335-A 32 20-JUN-1990;
Gruenthal GmbH
FEATURES Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
gene 1..321
/gene="ALP-237"
CDS 1..321
/gene="ALP-237"
/codon_start=1
/transl_table=11
/protein_id="CAA00746.1"
/db_xref="GI:413357"
/translations="SGKSPKAGVCPVKPKSAQCLRYKKPECQSDMQCPGKRCPCDTGCG
IKCLDPVDTFNPTRRKPGKPVYTGQCLLLNPNFCELDGQCKRDLKCCGLGFCGKSCV
SPVKA"
ORIGIN
Alignment Scores: 1.15e-38 Length: 321
Pred. No.: 621.00 Matches: 103
Score: 99.07% Conservative: 3
Percent Similarity: 96.26% Mismatches: 1
Best Local Similarity: 81.50% Indels: 0
Query Match: 6 Gaps: 0
DB: 6
US-10-613-105-2 (1-132) x A08110 (1-321)
Qy 26 SerGlyLysSerPheLysAlaGlyValCysProProLysLysSerAlaGlnCysLeuArg 45
Db 1 AGCGGTAAGTCTTTCAAAGCCGGCTGTCTCCTTAAGAAATCTGCTCAGTGCCTGCGT 60
Qy 46 TyrLysLysProGluCysGlnSerAspTTPGlnCysProGlyLysLysArgCysCysPro 65
Db 61 TACAAGNAACCCGAGTGCAGTCTGACTGCGAGTGTCTGTTAAGAACGCTTGTGTCTT 120
Qy 66 AspThrCysGlyLysCysLeuAspProValAspThrProAsnProThrArgArgLys 85
Db 121 GACACTTGTGTATCAATGCCCTGGATCGGTTGACACCCGACCGCGCTCGTAAA 180
Qy 86 ProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAsnProProAsnPheCys 105
Db 181 CCCGGGAAGTGCCTGATCGGTTACCTACGGTCACTGCTGCTGCTGCTGCTGCTGCTG 240
Qy 106 GluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGlyMetCysGlyLysSer 125
Db 241 GAGCTCGATGCCGAGTGCACCAACGAGATCTGAAATGCTGCTGCTGCTGCTGCTGCTG 300
RESULT 30
A08105
LOCUS A08105 321 bp DNA linear PAT 28-JUL-1993
DEFINITION Synthetic ALP-gene 230.
ACCESSION A08105
VERSION A08105.1 GI:413346
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 321)
AUTHORS Heinzel-Wieland,R., Ammann,J., Steffens,G.J. and Flohe,L.
TITLE Serine protease inhibitor proteins, medicaments containing them,
DNA sequences coding for these proteins and methods for producing
these proteins, medicaments and DNA sequences
JOURNAL Patent: EP 0373335-A 27 20-JUN-1990;
Gruenthal GmbH
FEATURES Location/Qualifiers


```

source
1. 2657
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
181..184
/notes="put. CAAT-box"
242..247
/notes="put. TATA-box"
276..2574
/notes="put. primary transcript of SLPI"
276..375
/notes="put. exon 1"
join(291..375,1092..1250,1668..1817,2397..2401)
/codon_start=1
/product="secretory leukocyte protease inhibitor (SLPI)"
/protein_id="CAA28187.1"
/db_xref="GI:758101"
/db_xref="GOA:P03973"
/db_xref="Swiss-Prot:P03973"
/translation="MKSSGLFPELVLLAGTLPMAVEGSGKSFKAGVCPPKKAQCL
RYKPKCQSDMOCFGRKRCPCDPTCGIKCLDPDVTNPNTRRKPGKCPVYGCCLMLNPP
NFCMDGQCKRDLKCCMGKSCVSPVKA"
291..365
/notes="signal peptide (AA -25 to -1)"
join(366..375,1092..1250,1668..1817,2397..2398)
/gene="SLPI"
/product="unnamed"
join(366..375,1092..1250,1668..1817,2397..2398)
/gene="SLPI"
376..1091
/notes="SLPI"
/notes="intron 1"
1092..1250
/gene="SLPI"
/notes="exon 2"
1251..1667
/notes="SLPI"
/notes="intron II"
1667..1817
/notes="SLPI"
/notes="exon 3"
1818..2396
/notes="SLPI"
/notes="intron III"
2397..2574
/notes="exon 4"
2549..2554
/notes="polyA signal"
2574
/notes="polyA site"

ORIGIN
Alignment Scores:
Pred. No.: 3,78e-32 Length: 2657
Score: 547.00 Matches: 109
Percent Similarity: 42.49% Conservative: 7
Best Local Similarity: 39.93% Mismatches: 11
Query Match: 71.78% Indels: 146
DB: 9 Gaps: 2

US-10-613-105-2 (1-132) x HSLIPG (1-2657)
QY 5 GlyLeuPheProPheLeuValLeuAlaLeuGlyThrLeu----- 18
Db 998 GGTCCTCCCCCTCAAAAGTGGCTTTGTTGAGGAGCATGGTCTCTAGTACCCA 1057
QY 19 ---AlaProTrpAlaValGluGlySerGlyLysSerPheLysAlaGlyValCysProPro 37
Db 1058 GCCTCCCTCCCTACCTCTTGACTTCTCTTCAAAAGCCTTCAAGCTGGAGTCTGCTCCT 1117
QY 38 LysLysSerAlaGlnCysLeuAlaGlyThrLysLysProGluCysGlnSerAspTrpGlnCys 57
Db 1118 AAGAAATCTGCCAGTGCCTTAGATACAGAAACCTGAGTGCAGAGTGTGCTGGCAGTGT 1177

```

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QY 58 ProGlyLysLysArgCysCysProAspThrCysGlyLysLysCysLeuAspProValAsp 77
Db 1178 CCAGGGAAGAAGAGATGTTGTCCTGACACTTGTGGCATCAATGCCTGGATCTGTTGAC 1237
QY 78 ThrProAsnProThr----- 82
Db 1238 ACCCAAAACCCAAAGTAAGCAGGTGCGGGAACTGGGGTAGAGAGATAGCTGGGACACAGC 1297
QY 82 ----- 82
Db 1298 ATTAGAGGACGGAACCTGGGTGATGGGTCTGCCAGGCCCTCTTGTCAATGCCGTAGTA 1357
QY 82 ----- 82
Db 1358 GTCACAGTGCCTTAAGAGAAGTAGCCAGCTGGTGAAGCAGCGGGCATTTAGATAGCCAGG 1417
QY 82 ----- 82
Db 1418 TAGTTGGAAGCCTCCACCTAGTACAGCATGTGGCGCGCTGGCACCTGCATATATGGGGGCC 1477
QY 82 ----- 82
Db 1478 TGAAGTTCTAGGAGAGCCAGGTGCTATGTTGGGGGCCGCCCTTAGGGAGAAGGTGGTGT 1537
QY 82 ----- 82
Db 1538 GATAGAGTGGGGAGGGAGTATGCCCTCTGTAAGCTGGACGAGGGGCTCACTCTAAA 1597
QY 82 ----- 82
Db 1598 AAGTGGGATGGAGGGGTTGTATAAAGTACAAAGGCCTCTGACCGGTAGCCTCACTCTCA 1657
QY 83 -----ArgArgLysProGlyLysCysProValThrTyrGlyGlnCysLeuMet 98
Db 1658 CCCAACCCAGCAAGGAGGAGCTGGGAAGTGCCAGTACTTATGGCCAATGTTTGATG 1717
QY 99 LeuAsnProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCys 118
Db 1718 CTTAACCCCCCAATTTCTGTGAGATGGATGGCAGTGCCAGTGAAGCGTGACTTGAAGTGTTC 1777
QY 119 MetGlyMetCysGlyLysSerCysValSerProValLys 131
Db 1778 ATGGGCATGTGGGAAATCCTGCGTTTCCCTGTGAAA 1816

RESULT 33
101501
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
ORIGIN
Alignment Scores:
Pred. No.: 9.86e-33 Length: 498

```

Score: 545.00 Matches: 90
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 71.52% Indels: 0
DB: 6 Gaps: 0

US-10-613-105-2 (1-132) x I01501 (1-498)

QY	43	CyeLeuArgTyrLysLysProGluCysGlnSerAspTrpGlnCysProGlyLysLysAAG	62
Db	25	TGCTTTAGATACAAAGAAACCTGAGTGCCAGAGTACTGGCAGTGTCCAGGGAAGAGAGA	84
QY	63	CysCysProAspThrCysGlyLysLysCysLeuAspProValAspThrProAsnProThr	82
Db	85	TGTTGCTGACACTGTGGCATCAATGCTGGATCTGTTGACACCCCAACCAACA	144
QY	83	ArgArgLysProGlyLysCysProValThrTyrGlyClnCysLeuMetLeuAsnProPro	102
Db	145	AGGAGGAAGCTGGGAAGTGCCAGTGACTATGGCAATGTTTGATGCTTAACCCCC	204
QY	103	AsnPheCysGluMetAspGlyGlnCysLeuArgAspLeuLysCysCysMetGlyMetCys	122
Db	205	AATTTCTGTGAGATGATGCCAGTGCAAGCGTGAAGTGTTCATGGGCATGTGT	264
QY	123	GlyLysSerCysValSerProValLysAla	132
Db	265	GGGAATCTGCTTCCCTGTTGAAAGCT	294

RESULT 34

HS30012/c

LOCUS

DEFINITION

Human DNA sequence from clone RP1-30012 on chromosome 20q12-13.12
Contains ESTs, GSSs and STSs. Contains part of a novel gene and the
SLPI gene for secretory leukocyte protease inhibitor
(antileukoproteinasel), complete sequence.

ACCESSION

AL035660

VERSION

1

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

HS30012 63796 bp DNA linear PRI 07-APR-2001
Human DNA sequence from clone RP1-30012 on chromosome 20q12-13.12
Contains ESTs, GSSs and STSs. Contains part of a novel gene and the
SLPI gene for secretory leukocyte protease inhibitor
(antileukoproteinasel), complete sequence.

AL035660.16 GI:11418457
HTG: antileukoproteinasel; proteinase inhibitor; SLPI.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 63796)
Ramsay, H.
Direct Submission
Submitted (29-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Nov 29, 2000 this sequence version replaced gi:10198630.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 20, constructed by the Sanger Centre Chromosome 20
Mapping Group. Further information can be found at
<http://www.sanger.ac.uk/HGP/Chr20>
IMPORTANT: This sequence is not the entire insert of clone
RP1-30012 it may be shorter because we sequence overlapping
sections only once, except for a 100 base overlap.
The true left end of clone RP3-453C12 is at 63697 in this sequence.
The true right end of clone RP1-172H20 is at 100 in this sequence.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred problems >=
30); an attempt was made to resolve all sequencing problems, such

as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. RP1-30012 is from the
library RP1-1 constructed by the group of Pieter de Jong. For
further details see
<http://www.chori.org/bacpac/home.htm>
VECTOR: pCYPAC2.

FEATURES

source

Location/Qualifiers

1..63796	/organism="Homo sapiens"
	/mol_type="genomic DNA"
	/db_xref="taxon:9606"
	/chromosomes="20"
	/map="q12-13.12"
	/clone="RP1-30012"
	/clone_lib="RP1-1"
251..554	/note="152 copies 2 mer aa 66% conserved"
253..556	/note="76 copies 4 mer aaga 66% conserved"
975..1059	/note="MIR repeat: matches 110..197 of consensus"
1143..1674	/note="L1M3 repeat: matches 5592..6164 of consensus"
1641..1934	/note="L1M4 repeat: matches 4935..5225 of consensus"
1939..2038	/note="L1M4 repeat: matches 5628..5728 of consensus"
2035..2766	/note="L1M4 repeat: matches 4215..4986 of consensus"
2764..3024	/note="L1M4 repeat: matches 1740..1979 of consensus"
3025..3316	/note="AluSg repeat: matches 1..293 of consensus"
3317..4149	/note="L1M4 repeat: matches 802..1740 of consensus"
join(5925..5993,6243..6400)	/gene="dJ30012.1"
join(5925..5993,6243..6400)	/gene="dJ30012.1"
	/product="dJ30012.1 (putative novel transcript)"
	/note="match: ESTs: Em:AI222267"
	/evidence="not_experimental"
6104..6223	/note="AluSg/x repeat: matches 174..298 of consensus"
7809..8022	/note="Charlie2 repeat: matches 3505..3724 of consensus"
8057..8416	/note="MER52C repeat: matches 894..1278 of consensus"
8417..9408	/note="t1 repeat: matches 2125..3119 of consensus"
9340..10314	/note="L1M2 repeat: matches 1213..2572 of consensus"
10328..10905	/note="L1M3 repeat: matches -125..225 of consensus"
	complement(11008..11364)
	/note="match: GSS: Em:AQ492607"
11229..11533	/note="L1M3 repeat: matches -477..-184 of consensus"
12038..12289	/note="MER1B repeat: matches 65..337 of consensus"
12290..12648	/note="L1M1 repeat: matches 1207..1574 of consensus"
	complement(12725..13141)
	/note="match: GSS: Em:AQ760198"
13052..13153	/note="MIR repeat: matches 33..137 of consensus"
13131..13392	/note="match: GSS: Em:AQ081155"
13218..13397	/note="45 copies 4 mer gaa 66% conserved"
13928..14216	/note="AluSx repeat: matches 1..310 of consensus"

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repeat_region 14372..14593
/notes="L1ME2 repeat: matches 5935..6162 of consensus"
repeat_region 14895..15168
/notes="AluX repeat: matches 5..295 of consensus"
misc_feature complement(14950..15573)
/notes="match: GSS: Em:AQ241185"
misc_feature 15703..16159
/notes="match: GSS: Em:AQ017550"
repeat_region 16175..16190
/notes="L1M4 repeat: matches 4145..4159 of consensus"
repeat_region 16191..16500
/notes="AluSq repeat: matches 2..310 of consensus"
repeat_region 16501..16608
/notes="L1M4 repeat: matches 4027..4145 of consensus"
repeat_region 16659..16839
/notes="MR97b repeat: matches 2..179 of consensus"
repeat_region 16847..17348
/notes="L1M4 repeat: matches 3473..4025 of consensus"
repeat_region 17616..19408
/notes="L1MB7 repeat: matches 4367..6167 of consensus"
repeat_region 19499..19670
/notes="86 copies 2 mer at 79% conserved"
repeat_region 19502..19689
/notes="42 copies 4 mer tata 79% conserved"
repeat_region 19678..21535
/notes="L1M4 repeat: matches 67..1979 of consensus"
repeat_region 21547..21682
/notes="Tigger4 (Zombi) repeat: matches 1..137 of consensus"
repeat_region 21690..22537
/notes="Tigger4 (Zombi) repeat: matches 1872..2730 of consensus"
repeat_region 22669..22996
/notes="L1M4 repeat: matches 3623..3953 of consensus"
repeat_region 23636..23896
/notes="L1M2 repeat: matches 1943..2572 of consensus"
repeat_region 23825..26024
/notes="L1 repeat: matches 2121..4337 of consensus"
misc_feature 25994..26445
/notes="match: GSS: Em:AQ470847"
repeat_region 26025..26160
/notes="L1R13 repeat: matches 796..936 of consensus"
repeat_region 26161..26235
/notes="L1 repeat: matches 5112..5188 of consensus"
misc_feature 26204..26681
/notes="match: GSS: Em:AQ624124"
misc_feature complement(27205..27381)
/notes="match: STS: Em:G06121"
gene complement(27206..29528)
/genes="SLPI"
mRNA complement(join(27206..27386,27969..28118,28542..28700,
29426..29528))
/genes="SLPI"
/product="d3J0012.2 (secretory leukocyte protease
inhibitor (antileukoprotease))"
/notes="match: cDNAs: Em:U88093 Em:X04470 Em:U73004
Em:X04503 Em:M57446 Em:U94341 Em:AF151982 Em:AF178426
Em:AF114471 Em:M31216
match: ESTs: Em:R71834 Em:AA683520 Em:AA316675 Em:AI742512
Em:AA572950 Em:AA564454 Em:AI862145 Em:AI540954
Em:AI638119 Em:AI222907 Em:AI743345 Em:AW081599
Em:AW264225 Em:AA460433 Em:AI885550 Em:AW238407
Em:AI564623 Em:AA541595 Em:AA132992 Em:H65117 Em:AA397776
Em:AA93549 Em:AI377093 Em:AA165295 Em:AW190157
Em:AA557989 Em:RA164414 Em:H65171 Em:N27733 Em:AW103765
Em:AA460434 Em:RA49913 Em:AA026192 Em:AW391622 Em:T28664
Em:AA026099 Em:AA026497 Em:AA485776 Em:AI247078
Em:AI276322 Em:AI367954 Em:AI826892"
/evidence=not_experimental
polya_site complement(27206)
/genes="SLPI"
polya_signal complement(27226..27231)
/genes="SLPI"
repeat_region 27229..27315

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polya_signal /note="L2 repeat: matches 2627..2710 of consensus"
complement(27230..27235)
/genes="SLPI"
CDS complement(join(27382..27386,27969..28118,28542..28700,
29426..29510))
/genes="SLPI"
/note="match: proteins: Tr:O44397 Sw:P03973 Tr:Q9WUQ4
Sw:P97430 Tr:Q9R0Z8 Tr:O95959 Sw:P09412 Sw:P22298
Tr:Q9XS44"
/codon_start=1
/evidence=not_experimental

Alignment Scores:
Pred. No.: 4..9e-30 Length: 63796
Score: 537.50 Matches: 103
Percent Similarity: 42.51% Conservative: 2
Best Local Similarity: 41.70% Mismatches: 1
Query Match: 70.54% Indels: 141
DB: 9 Gaps: 1

US-10-613-105-2 (1-132) x HS30012 (1-63796)
QY 26 SerGlyLysSerPheLysAlaGlyValCysProLysLysSerAlaGlnCysLeuAtg 45
DB 28710 TCTTCAAAAGCCTCAAGCTGGAGTCTGTCTCTTAAGAAATCTGCCAGTGCCTTAGA 28651
QY 46 TyrLysLysProGluCysGlnSerAspTrpGlnCysProGlyLysLysArgCysCysPro 65
DB 28650 TACAGAAACCTGAGTGCAGAGTGACTGCAGTGTCCAGGGGAAGAAGATGTTGTCT 28591
QY 66 AspThrCysGlyLysLysCysLeuAspProValAspThrProAsnProThr----- 82
DB 28590 GACACTTGTGGCATCAATGCTGGATCTCTGTGACACCCCAACCAAGTAAGCAGGTC 28531
QY 82 ----- 82
DB 28530 GGGGAACTGGGTAGAGAGGAGTGAGCCTGGGACACAGCATTAGAGGGGATGGAACCTGGGT 28471
QY 82 ----- 82
DB 28470 GATGGGTCTGCCAGGSCCTCTTGTCAATCCGTCAGTGAGTCACACTGCCCTTAAGCAGGA 28411
QY 82 ----- 82
DB 28410 AGGTAGCCAGCAGCTGGTGAAGCAGCGGCGCATTTAGATAGCCAGGTAGTTGGAAGCCTCC 28351
QY 82 ----- 82
DB 28350 CACCTAGTCAGCACTGGGTGGCTGGCCACCTGCATCAATGGGGGGGCTGAAGTTCATAGGA 28291
QY 82 ----- 82
DB 28290 GAGCCAGGTGCTATGTTTGGGGGCCCTTAGGAGAGAGTGGTGGTATAGAGTGGGG 28231
QY 82 ----- 82
DB 28230 AGGGATGATCCCCCTGCTGAAGCTGGAGCAGGGGCTCACTCTAAAAAGTGGGGATGGG 28171
QY 83 -----AtgAtg 84
DB 28170 AGGGGTGTATAAAGTACAAAGGCTCTGACCGGTAGCCTCACTCTCACCCAGCAAGAGG 28111
QY 85 LysProGlyLysCysProValThrTyrGlyGlnCysLeuMetLeuAsnProProAsnPhe 104
DB 28110 AGCCTGGGAAGTGGCCAGTGACTTATGGCAATGTTTGTATGTTTAAACCCCAATTTC 28051
QY 105 CysGluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGlyMetCysGlyLys 124
DB 28050 TGTGAGATGGATGGCCAGTGCAGAGCGTGACTTGAAGTGTTCATGGGCATGTGTGGGAAA 27991
QY 125 SerCysValSerProValLys 131
DB 27990 TCCTGCTTTCCCTCTGTGAAA 27970

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RESULT 35
LOCUS   FIGALP               600 bp      mRNA      linear      MAM 07-MAR-1995
DEFINITION Porcine antileukoprotease mRNA, complete cds.
ACCESSION M57446
VERSION   M57446.1 GI:164319
KEYWORDS  antileukoprotease.
SOURCE    Sus scrofa (pig)
ORGANISM  Sus scrofa
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 600)
AUTHORS   Farmer,S.J., Fliss,A.E. and Simmen,R.C.
TITLE      Complementary DNA cloning and regulation of expression of the
            messenger RNA encoding a pregnancy-associated porcine uterine
            protein related to human antileukoprotease
JOURNAL   Mol. Endocrinol. 4 (8), 1095-1104 (1990)
MEDLINE   91155942
PUBMED    2293019
COMMENT   Original source text: Porcine uterus. cdna to mRNA, clone pALP.
FEATURES
     source
         1..600
         /location="uterus"
         /organism="Sus scrofa"
         /mol_type="mRNA"
         /db_xref="taxon:9823"
         /clone="pALP"
         /sex="female"
         /tissue_type="uterus"
     gene
         1..600
         /gene="ALP"
         44..391
         /gene="ALP"
         /codon_start=1
         /product="antileukoprotease"
         /protein_id="AAA63446.1"
         /db_xref="GI:164320"
         /translations="MAPWAVEGAENALKGACPPRKIVOCRLRVEKPKCTSDWQCPDKK
            KCCRDTCALKCLNPVATNPVKPKCPVYQCMMLPPNPHCKTDSQCLGDLKCK
            SMCCKVCLTPVKA"
     polyA_site
         600
         /gene="ALP"
     ORIGIN
Alignment Scores:
Pred. No.:      6,81e-30      Length:      600
Score:          508.50      Matches:      87
Percent Similarity: 78.29%      Conservative: 14
Best Local Similarity: 67.44%      Mismatches:  26
Query Match:    66.73%      Indels:       2
DB:             4           Gaps:         1

US-10-613-105-2 (1-132) x FIGALP (1-600)

QY      5 GlyLeuPheProPheLeuValLeuAlaLeuGly-ThrLeuAlaProTrpAlaValGl 24
Db      7 GGCTCTTGCCCTTC---GTGCTTCTGCCCTGGGAATCATGCACCTTGGCCGTGGA 63
QY      24 uGlySerGlyLysSerPheLysAlaGlyValCysProProLysLysSerAlaGlnCysLe 44
Db      64 AGGTGCTGAAATGCTTTGAAAGGGGGAGCGTGCCTCTCTAGAAAATTTGCCAGTGCCT 123
QY      44 uAGTGTyRLysLeuProGluCysGlnSerAspTrpGlnCysProGlyLysLysArgCysCy 64
Db      124 TAGATATGAGAAACCCCAAGTGCACAGTGTACTGGCAGTGTCCAGAACGAAGAATGTTG 183
QY      64 sProAspThrCysGlyLysLysCysLeuAspProValAspThrProAsnProThrArgAr 84
Db      184 CCAGATACTTGGCAATCAATGCCCTGAACCTCTGTGCTATCACGACCCAGTTAAGGT 243
QY      84 gLysProGlyLysCysProValThrTyRGlyGlnCysLeuMetLeuAsnProProAsnPh 104
Db      244 GAAGCCTGGGAAGTGTCCAGTGGTCTATGGCCAGTGTATGATGTCTCAACCCCAATCA 303

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QY      104 eCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCysMetGlyMetCysGlyLy 124
Db      304 CTGCAAGACAGACAGCAGTCGCTGGTGACTTAAATGCTGCAAGAGCATGTGCGGAA 363
QY      124 sSerCysValSerProValLysAla 132
Db      364 AGTCGTGCTCACCCCTGTGAAAGCC 388

RESULT 36
LOCUS   AF178426             490 bp      mRNA      linear      ROD 29-AUG-1999
DEFINITION Rattus norvegicus secretory leukocyte protease inhibitor mRNA,
            complete cds.
ACCESSION AF178426
VERSION   AF178426.1 GI:5802679
KEYWORDS  Rattus norvegicus (Norway rat)
ORGANISM  Rattus norvegicus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
          Rattus.
REFERENCE 1 (bases 1 to 490)
AUTHORS   Song,X., Zeng,L., Jin,W., Thompson,J., Mizel,D.E., Lei,K.,
            Billinghamst,R.C., Poole,A.R. and Wahl,S.M.
TITLE      Secretory leukocyte protease inhibitor suppresses the inflammation
            and joint damage of bacterial cell wall-induced arthritis
JOURNAL   J. Exp. Med. 190 (4), 535-542 (1999)
MEDLINE   99380355
PUBMED    10449524
REFERENCE 2 (bases 1 to 490)
AUTHORS   Song,X.-Y. and Zeng,L.
TITLE      Direct Submission
JOURNAL   Submitted (17-AUG-1999) Oral infection & Immunity Branch, National
            Institute of Dental & Craniofacial research, 9000 Rockville Pike,
            Bethesda, MD 20892
FEATURES
     source
         1..490
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Alignment Scores:
Pred. No.:      5.11e-28      Length:      490
Score:          482.50      Matches:      83
Percent Similarity: 75.00%      Conservative: 16
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Query Match:    63.32%      Indels:       3
DB:             10          Gaps:         2

US-10-613-105-2 (1-132) x AF178426 (1-490)

QY      1 MetLysSerSerGlyLeuPheProPheLeuValLeuAlaLeuGlyThrLeuAlaPro 20
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QY      21 TrpAlaValGluGlySerGlyLys-----SerPheLysAlaGlyValCysProProLys 38
Db      69 TGGAGTGTGGAGGA---GGCAAAATGATGATCTATCAAAATTTGGAGCCTGCCCTGTGCTAGA 125
QY      39 LysSerAlaGlnCysLeuArgTyRLysLysProGluCysGlnSerAspTrpGlnCysPro 58

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Db	126	AAGCCTGCCAGTGCCTTAAACTTGAGAAACCAAGAGTGGGTACTGACTGGGAATGCCCA	185
QY	59	GLYLYSArgCysCysProAspThrCysGlyLeuValLeuAlaLeuGlyThrLeuAlaPro	78
Db	186	GGAAAGCAGAGATGCTGCCAAGATACTGTGGTTCAAGTGCCTGAATCCTGTTCCTT	245
QY	79	ProAsnProThrArgArgLysProGlyLysCysProValThrTyrGlyGlnCysLeuMet	98
Db	246	CGTGGACCAAGTGAAGAAGACCTGGGAGTGGCTCAAAATTTCAAGGAAAATGCTGATG	305
QY	99	LeuAsnProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCys	118
Db	306	CTTAAACCTCCCAATAGTCCAGATGACGGCAGTGTGATGGCAAAATACAAATGTGT	365
QY	119	MetGlyMetCysGlyLysSerCysValSerProVal	130
Db	366	GAGGGCATGTGTGGGAAAGTCTGCCTTCCCCAGT	401
RESULT 37			
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LOCUS		Rattus norvegicus secretory leukocyte protease inhibitor (SLPI)	
DEFINITION		mRNA, complete cds.	
ACCESSION	AF151982	GI:4929548	
VERSION			
KEYWORDS			
SOURCE		Rattus norvegicus (Norway rat)	
ORGANISM		Rattus norvegicus	
REFERENCE		1 (bases 1 to 667)	
AUTHORS		Chen,D., Xu,X., Cheon,Y.P., Bagchi,M.K. and Bagchi,I.C.	
TITLE		Estrogen Induces Expression of Secretory Leukocyte Protease Inhibitor in Rat Uterus	
JOURNAL		Biol. Reprod. 71 (2), 508-514 (2004)	
PUBMED		15044260	
REFERENCE		2 (bases 1 to 667)	
AUTHORS		Chen,D.H., Xu,X.P., Bagchi,M.K. and Bagchi,I.C.	
TITLE		Molecular cloning and spatio-temporal expression of rat secretory leukocyte protease inhibitor (SLPI) in the uterus	
JOURNAL		Unpublished	
REFERENCE		3 (bases 1 to 667)	
AUTHORS		Chen,D.H., Xu,X.P., Bagchi,M.K. and Bagchi,I.C.	
TITLE		Direct Submission	
JOURNAL		Submitted (17-MAY-1999) Center for Biomedical Research, The Population Council, 1230 York Avenue, New York, NY 10021, USA	
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ORIGIN			
Alignment Scores:			
Prod. No.:	5.16e-27	Length:	667
Score:	471.00	Matches:	84
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Best Local Similarity:	63.64%	Mismatches:	30
Query Match:	61.81%	Indels:	4

Db	10	Gaps:	3
US-10-613-105-2 (1-132) x AF151982 (1-667)			
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QY	21	TpAlaValGluGlySerGlyLys-----SerPheLysAlaGlyValCysProProLys	38
Db	73	TGGAGTGTGGAGGA---GGCAAAATATGCTATCAAAATCGAGGCTGCTGTCTAGA	129
QY	39	LysSerAlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAspTrpGlnCysPro	58
Db	130	AAGCTGCCAGTGCCTTAAACGTCGAGAAACAGAGTGCAGTACTGACGGGATGCCCA	189
QY	59	GlyLysLysArgCysCysProAspThrCysGlyLysGlyLysCysLeuAspProValAsp	78
Db	190	GGAAAGCAGAGATGCTGCCAAGATACCTGTGGTTTCAAAATGCTGAATCCTGTTCCT	249
QY	79	ProAsnProThrArgArgLysProGlyLysCysProValThrTyrGlyGlnCysLeuMet	98
Db	250	CGTGGACCAAGT---AAGAAGCTGGGAGTGCCTCAAAATTTCAAGGAAAATGCTGATG	306
QY	99	LeuAsnProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCys	118
Db	307	CTTAAACCTCCCAATAGTCCAGATGACGGCAGTGTGATGGCAAAATACAAATGTGT	366
QY	119	MetGlyMetCysGlyLysSerCysValSerProVal	130
Db	367	GAGGGTATGTGTGGGAAAGTCTGCCTTCCCCAGT	402
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LOCUS		Rattus norvegicus secretory leukocyte protease inhibitor precursor,	
DEFINITION		mRNA, complete cds.	
ACCESSION	AF421377	GI:23451267	
VERSION			
KEYWORDS		Rattus norvegicus (Norway rat)	
SOURCE		Rattus norvegicus	
ORGANISM		Rattus norvegicus	
REFERENCE		1 (bases 1 to 680)	
AUTHORS		Wang,X., Li,X., Xu,L., Zhan,Y., Yaish-Ohad,S., Barone,F.C. and Feuerstein,G.Z.	
TITLE		Secretory Leukocyte Protease Inhibitor (SLPI) Upregulation in Cerebral Stroke: Expression of SLPI Protects Brain from Ischemic Injury	
JOURNAL		Unpublished	
REFERENCE		2 (bases 1 to 680)	
AUTHORS		Wang,X.	
TITLE		Direct Submission	
JOURNAL		Submitted (19-SEP-2001) Cardiovascular Sciences, DuPont Pharmaceuticals, Rt. 141 Experimental Station, B400/3418, Wilmington, DE 19880, USA	
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Db      279  AAGCTGCCAGTGCCTTAAGCTTGAGAACCAATGCCGACTACTGACTGGAGTGCCTCG 220
Qy      59   GlyLysLysArgCysCysProAspThrCysGlyLysCysLysLeuAspProValAspThr  78
Db      219  GGAAGCAGAGGTGCTGCCAAGATGCTTGGCGTTCCAAAGTGCCTGAATCCTGTTCCCAT 160
Qy      79   ProAsnProThrArgArgLysProGlyLysCysProValThrTyrGlyGlnCysLeuMet  98
Db      159  CGCAAAACCATGTGGAGAGCCTGGGAGTGCCTCAAAACTCAGCAAGATGTATGATG 100
Qy      99   LeuAsnProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCys 118
Db      99   CTTAACCTCCCAATGCTCTGCCAGAGGACGGGACGTGTGACGGCAATACAAAGTCTGT 40
Qy      119  MetGlyMetCysGlyLysSerCysValSerProVal 130
Db      39   GAGGATATATGTGGAAAGTCTGCTGCCCCCGATG 4
RESULT 41
AX577885
LOCUS      AX577885
DEFINITION Sequence 7 from Patent WO02081745.
ACCESSION AX577885
VERSION   AX577885.1 GI:27647093
KEYWORDS
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
REFERENCE 1
AUTHORS   Garcia,T., Roman Roman,S., Baron,R., Call,K., Theilhaber,J.,
          Connolly,T., Jackson,A., Bushnell,S.E. and Rawadi,G.
          Genes involved in osteogenesis, and methods of use
          Patent: WO 02081745-A 7 17-OCT-2002;
          Aventis Pharma S.A. (FR)
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Alignment Scores:
Pred. No.: 1.16e-26 Length: 409
Score: 463.50 Matches: 79
Percent Similarity: 72.73% Conservative: 17
Best Local Similarity: 59.85% Mismatches: 33
Query Match: 60.83% Indels: 3
DB: 6 Gaps: 2
US-10-613-105-2 (1-132) x AX577885 (1-409)
Qy      1   MetLysSerSerGlyLeuPheProPheLeuValLeuAlaLeuGlyThrLeuAlaPro 20
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Qy      21   TrpAlaValGluGlySerGlyLys-----SerPheLysAlaGlyValCysProProLys 38
Db      69   TGGACTGTGGAAGGA---GGCAAAATGATGCTATCAAAATCGGAGCCTGCCCTGCTATAA 125
Qy      39   LysSerAlaGlnCysLeuArgTyrLysLysProGluCysGlnSerAspTyrGlnCysPro  58
Db      126  AAGCTGCCAGTGCCTTAAGCTTGAGAACCAATGCCGACTACTGACTGGAGTGCCTCG 185
Qy      59   GlyLysLysArgCysCysProAspThrCysGlyLysCysLysLeuAspProValAspThr  78
Db      186  GGAAGCAGAGGTGCTGCCAAGATGCTTGGCGTTCCAAAGTGCCTGAATCCTGTTCCCAT 245
Qy      79   ProAsnProThrArgArgLysProGlyLysCysProValThrTyrGlyGlnCysLeuMet  98

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Db      246  CGCAAAACCATGTGGAGAGCCTGGAGTGCCTCAAAACTCAGCAAGATGTATGATG 305
Qy      99   LeuAsnProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCys 118
Db      306  CTTAACCTCCCAATGCTCTGCCAGAGGACGGGACGTGTGACGGCAATACAAAGTGTGT 365
Qy      119  MetGlyMetCysGlyLysSerCysValSerProVal 130
Db      366  GAGGATATATGTGGAAAGTCTGCTGCCCCCGATG 401
RESULT 42
MMU88093
LOCUS      MMU88093
DEFINITION Mus musculus secretory leukocyte protease inhibitor mRNA, complete cds.
ACCESSION U88093
VERSION   U88093.1 GI:1945382
KEYWORDS
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
REFERENCE 1
AUTHORS   Zitnik,R.J., Zhang,J., Kashem,M.A., Kohno,T., Lyons,D.E.,
          Wright,C.D., Rosen,E., Goldberg,I. and Hayday,A.C.
          The cloning and characterization of a murine secretory leukocyte
          protease inhibitor cDNA
          Biochem. Biophys. Res. Commun. 232 (3), 687-697 (1997)
          97271386
          PUBMED 9126337
REFERENCE 2 (bases 1 to 671)
AUTHORS   Zitnik,R.J., Zhang,J., Kashem,M.A., Kohno,T., Lyons,D.E.,
          Wright,C.D., Rosen,E., Goldberg,I. and Hayday,A.C.
          Direct Submission
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          Cedar Street, New Haven, CT 06520, USA
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ORIGIN
Alignment Scores:
Pred. No.: 1.91e-26 Length: 671
Score: 463.50 Matches: 79
Percent Similarity: 72.73% Conservative: 17
Best Local Similarity: 59.85% Mismatches: 33
Query Match: 60.83% Indels: 3
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US-10-613-105-2 (1-132) x MMU88093 (1-671)
Qy      1   MetLysSerSerGlyLeuPheProPheLeuValLeuAlaLeuGlyThrLeuAlaPro 20
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Qy      21   TrpAlaValGluGlySerGlyLys-----SerPheLysAlaGlyValCysProProLys 38
Db      73   TGGACTGTGGAAGGA---GGCAAAATGATGCTATCAAAATCGGAGCCTGCCCTGCTATAA 129
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Db      130  AAGCCTGCCAGTGCCTTAAGCTTGAGAGCAATGCCGTACTGACTGGAGTCCCG 189
Qy      59  GlyLysLysArgCysCysProAspThrCysGlyLysCysLeuAspProValAspThr 78
Db      190  GGAACGACGAGGCTGCCAAGATGCTTGGGTTCCAGTGGTGAATCTGTTCCTTCCATT 249
Qy      79  ProAsnProThrArgArgLysProGlyLysCysProValThrTyrglyGlnCysLeuMet 98
Db      250  CGCAAAACCAAGTGTGGAGGAAGCTGGAGTGGTCAAAACTCAGCAAGATGATGATG 309
Qy      99  LeuAsnProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCys 118
Db      310  CTTAACCCCTCCCAATCTCTGCCAGAGGAGCGGCAGTGTGACGGCAATACACAGTCTGT 369
Qy      119  MetGlyMetCysGlyLysSerCysValSerProVal 130
Db      370  GAGGGTATATGTGGAAAGTCTGCCTGCCCCCGATG 405

RESULT 43
MMU94341
LOCUS      682 bp mRNA linear ROD 29-OCT-1997
DEFINITION Mus musculus secretory leukoprotease inhibitor mRNA, complete cds.
ACCESSION U94341
VERSION   U94341.1 GI:1945450
KEYWORDS .
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 682)
AUTHORS   Abe,T., Toninaga,Y., Kikuchi,T., Watanabe,A., Satoh,K., Watanabe,Y.
           and Nukiwa,T.
TITLE     Bacterial pneumonia causes augmented expression of the secretory
           leukoprotease inhibitor gene in the murine lung
JOURNAL   Am. J. Respir. Crit. Care Med. 156 (4 Pt 1), 1235-1240 (1997)
MEDLINE   98011992
PUBMED    9351627
REFERENCE 2 (bases 1 to 682)
AUTHORS   Abe,T., Toninaga,Y., Kikuchi,T., Watanabe,A., Satoh,K., Watanabe,Y.
           and Nukiwa,T.
TITLE     Direct Submission
JOURNAL   Submitted (18-MAR-1997) Department of Respiratory Oncology and
           Molecular Medicine, Institute of Development, Aging and Cancer,
           Tohoku University, 4-1 Seiryomachi, Aoba-ku, Sendai 980-77, Japan
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ORIGIN
Alignment Scores:
Pred. No.: 1.94e-26 Length: 682
Score: 463.50 Matches: 79
Percent Similarity: 72.73% Conservative: 17
Best Local Similarity: 59.85% Mismatches: 33
Query Match: 60.83% Indels: 3
DB: 10 Gaps: 2

US-10-613-105-2 (1-132) x MMU94341 (1-682)
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Db      74  TGAAGTGTGGAAGGA---GGCAAAATGATGCTATCAAAATCGAGCCTGCCCTGCTTAA 130
Qy      39  LysSerAlaGlnCysLeuArgTyrglyLysProGluCysGlnSerAspTrpGlnCysPro 58
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Qy      59  GlyLysLysArgCysCysProAspThrCysGlyLysCysLeuAspProValAspThr 78
Db      191  GGAAGACGAGAGTGTGCCAAGATCTTGGGTTCCAGTGGTGAATCTGTTCCTTCCATT 250
Qy      79  ProAsnProThrArgArgLysProGlyLysCysProValThrTyrglyGlnCysLeuMet 98
Db      251  CGCAAAACCAAGTGTGGAGGAAGCTGGAGTGGTCAAAACTCAGCAAGATGATGATG 310
Qy      99  LeuAsnProProAsnPheCysGluMetAspGlyGlnCysLysArgAspLeuLysCysCys 118
Db      311  CTTAACCCCTCCCAATGTCTGCCAGAGGAGCGGCAGTGTGACGGCAATACACAGTCTGT 370
Qy      119  MetGlyMetCysGlyLysSerCysValSerProVal 130
Db      371  GAGGGTATATGTGGAAAGTCTGCCTGCCCCCGATG 406

BC028509      894 bp mRNA linear ROD 30-JUN-2004
Mus musculus secretory leukocyte peptidase inhibitor, mRNA (CDNA
clone MGC:41142 IMAGE:1513866), complete cds.
BC028509
ACCESSION    BC028509.1 GI:20306995
VERSION      BC028509
KEYWORDS     MGC.
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus
REFERENCE    1 (bases 1 to 894)
AUTHORS      Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
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            Butlerfield,Y.S., Krzywinski,M.I., Skalska,U., Smalins,D.E.,
            Scherch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
            Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
            Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
            12477932
            2 (bases 1 to 894)
            Strausberg,R.
            Direct Submission
            Submitted (23-APR-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
            NIH-MGC Project URL: http://mgc.nci.nih.gov
            Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Marcello Bento Soares, Ph.D.

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cDNA Library Preparation: M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Genome Sequence Centre,
 BC Cancer Agency, Vancouver, BC, Canada
 info@bcsc.bc.ca
 Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
 Andy Chan, Steve S. Chand, William Chow, Allison Cloutier, Ruth
 Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
 Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
 Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu,
 Parvaneh Saeedi, JR Santos, Angeliue Schnerch, Ursula Skalska,
 Duane Smalius, Jeff Scott, Miranda Tsai, George Yang, Jacque
 Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAC Plate: 67 Row: j Column: 6
 This clone was selected for full length sequencing because it
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CDS

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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 1123)
 AUTHORS Jin, F.Y., Nathan, C., Radzioch, D. and Ding, A.
 TITLE Secretory leukocyte protease inhibitor: a macrophage product
 induced by and antagonistic to bacterial lipopolysaccharide
 JOURNAL Cell 88 (3), 417-426 (1997)
 MEDLINE 97191310
 PUBMED 9039268
 REFERENCE 2 (bases 1 to 1123)
 AUTHORS Ding, A., Jin, F.-Y. and Nathan, C.F.
 TITLE Direct Submission
 JOURNAL Submitted (01-OCT-1996) Medicine, Cornell University Medical
 College, 1300 York Ave. Box 57, New York, NY 10021, USA
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